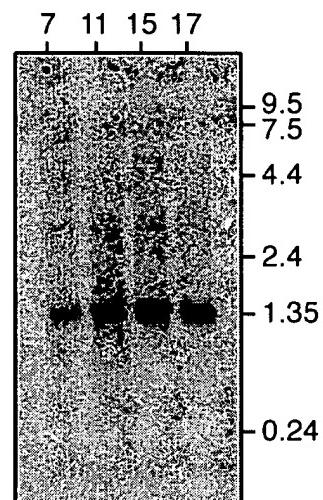
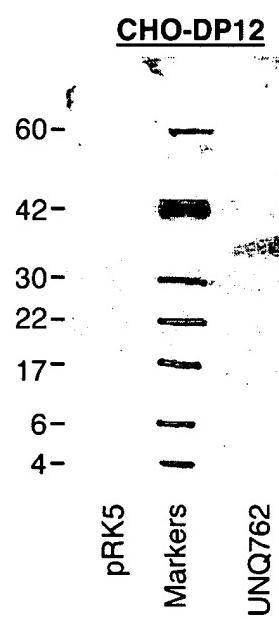
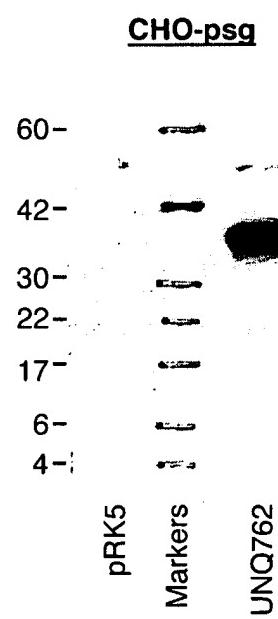
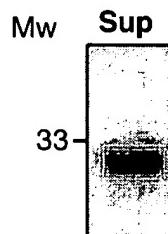
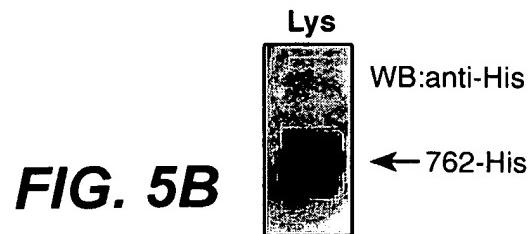
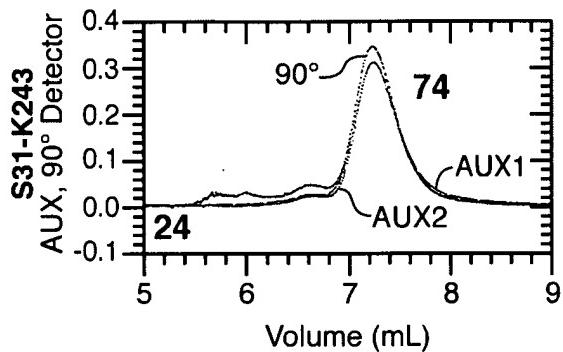
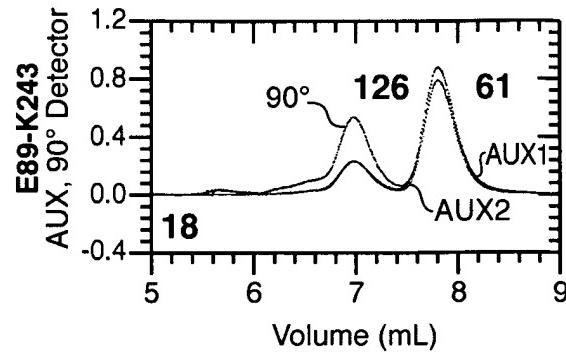
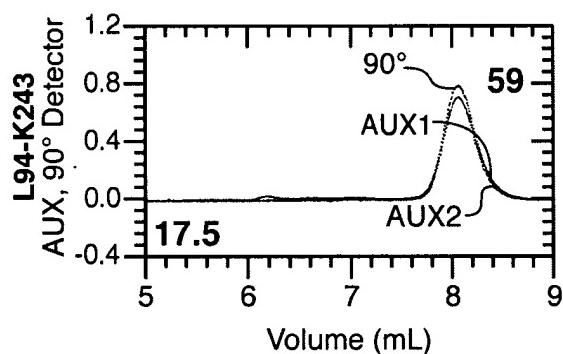
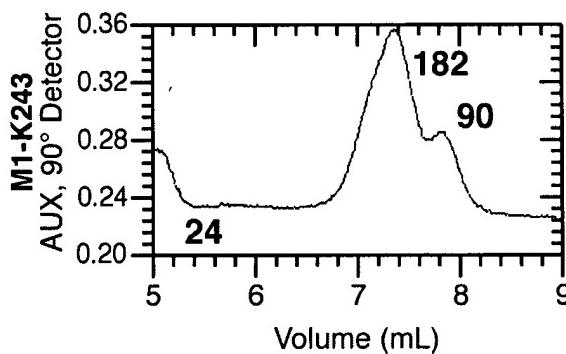
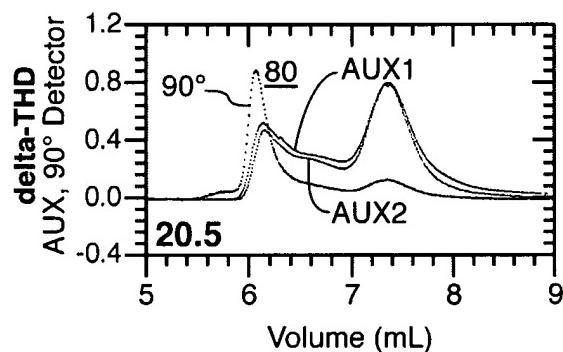
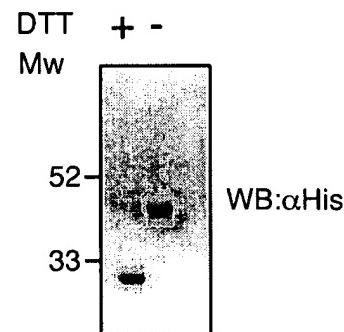
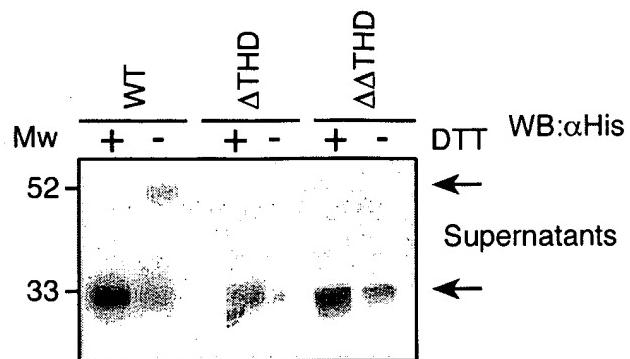
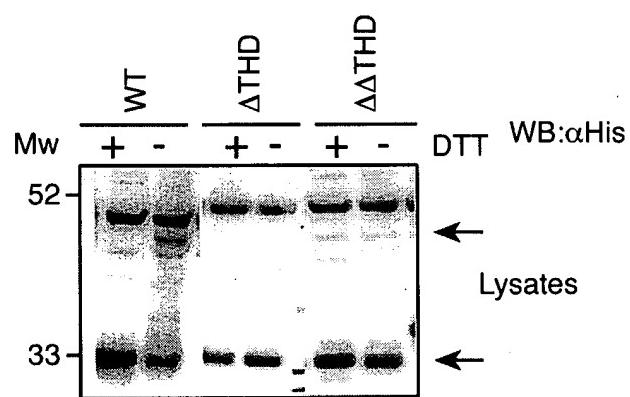
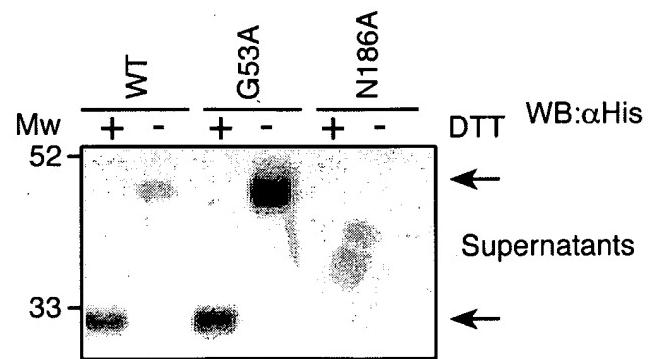
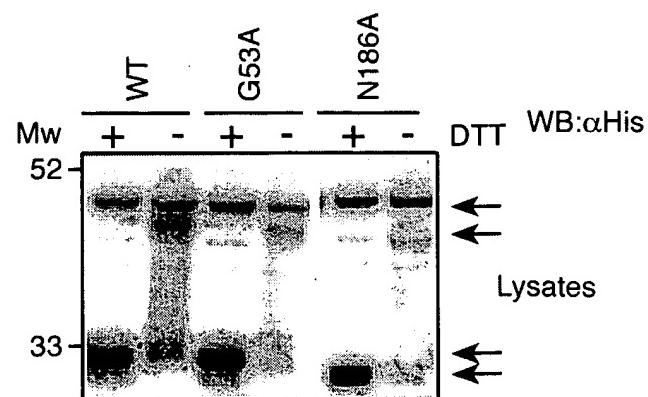
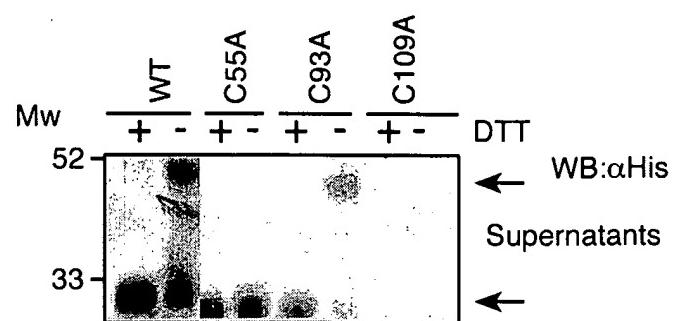
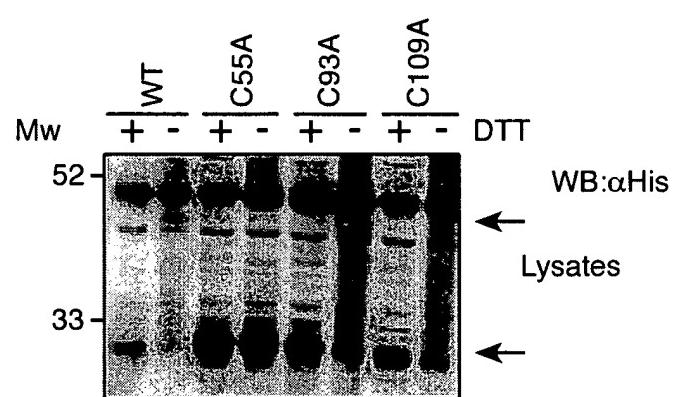
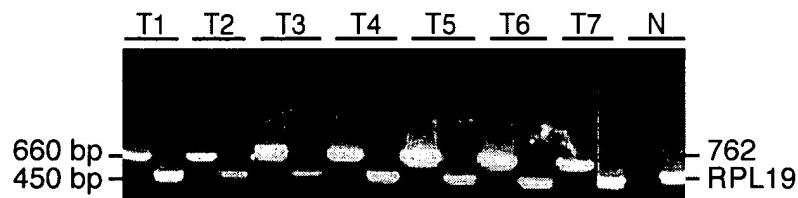
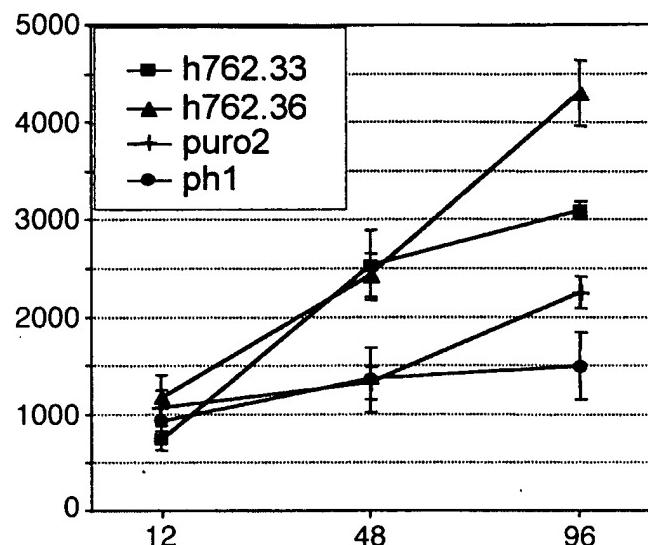
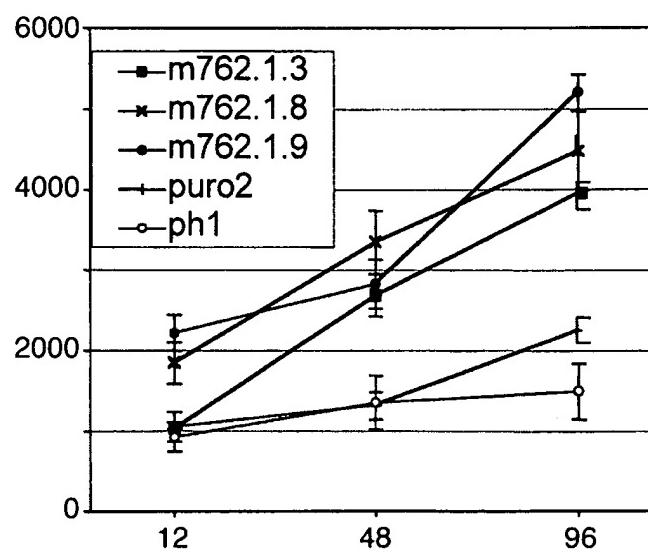
**FIG. 3A****Embryonic Days****FIG. 3B****FIG. 4A****FIG. 4B****FIG. 5A****FIG. 5B**

**FIG. 6A****FIG. 6B****FIG. 6C****FIG. 7A****FIG. 7B****FIG. 7C**

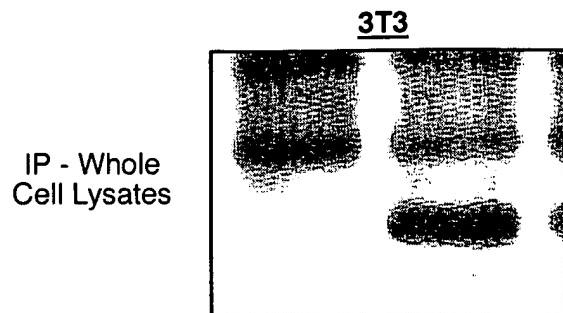
**FIG. 8A****FIG. 8B****FIG. 9A****FIG. 9B**

**FIG. 10A****FIG. 10B****FIG. 11**

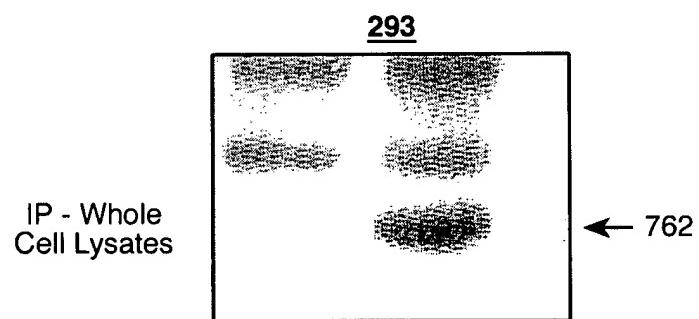
**FIG. 12A****FIG. 12B**

P5104R1

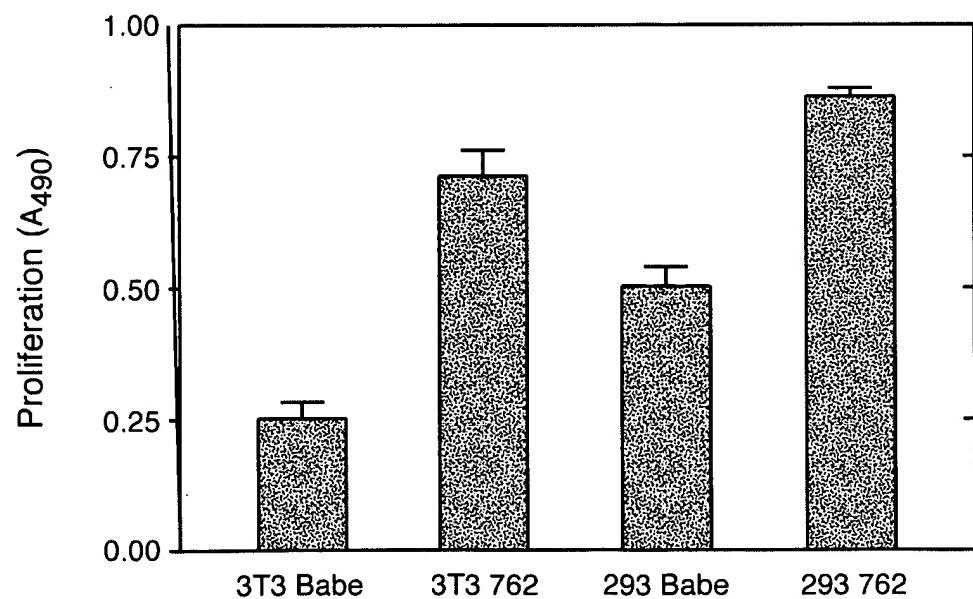
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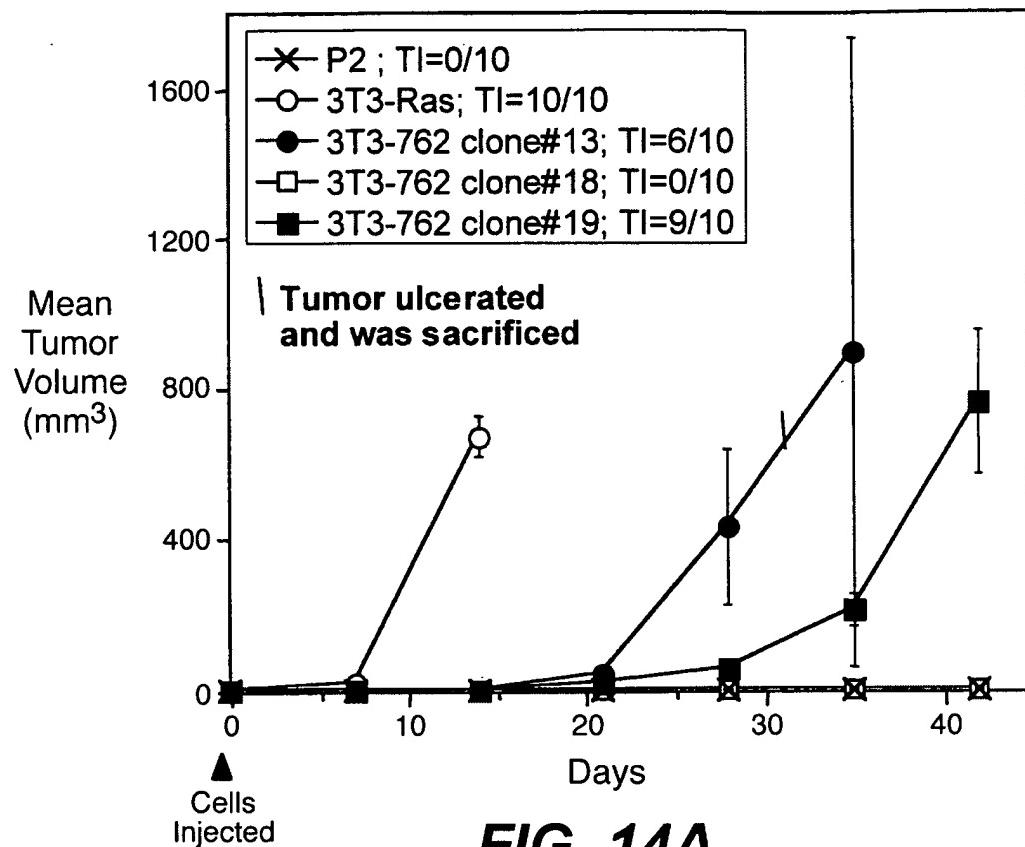
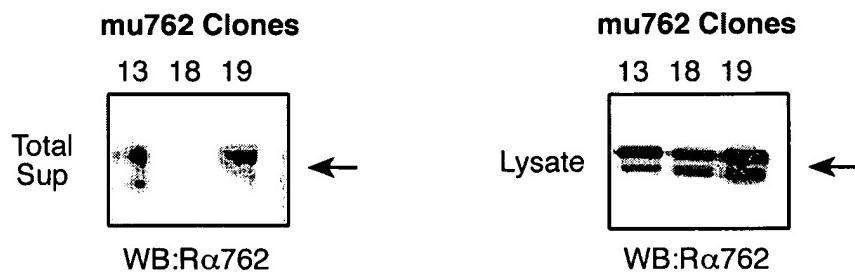
**FIG. 13A**



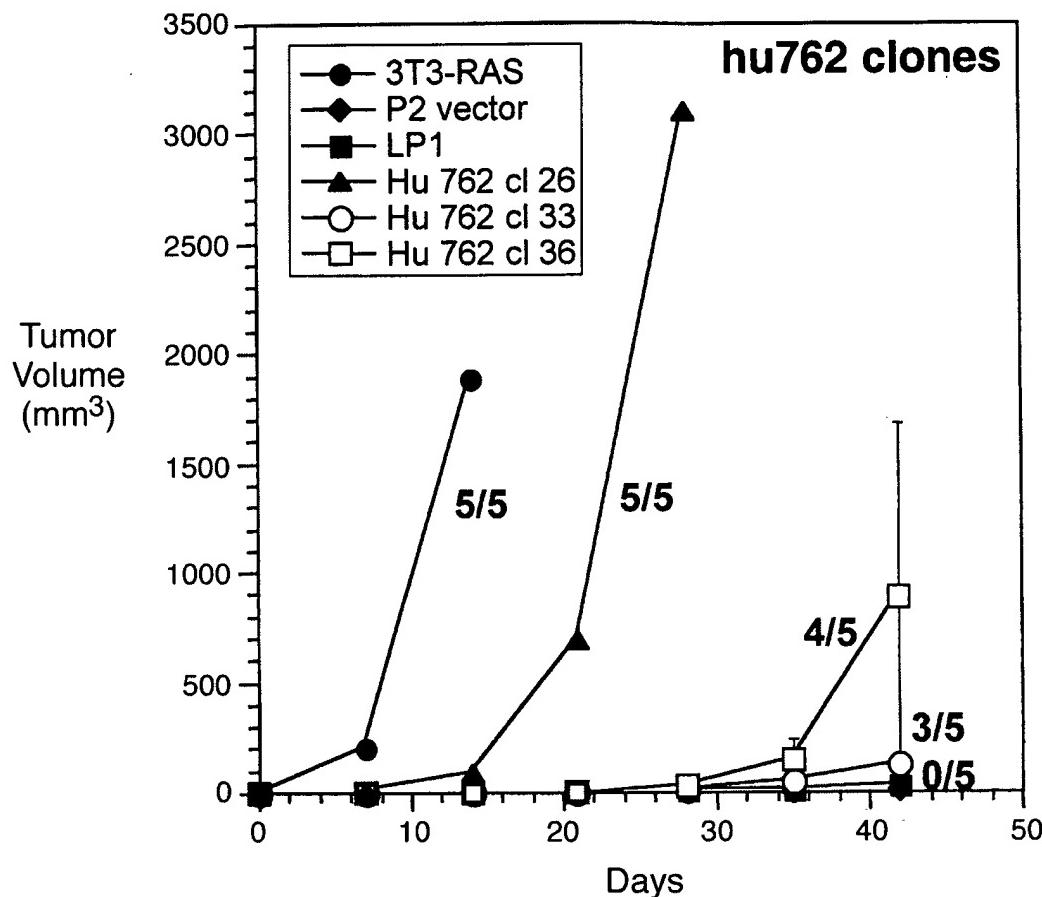
**FIG. 13B**

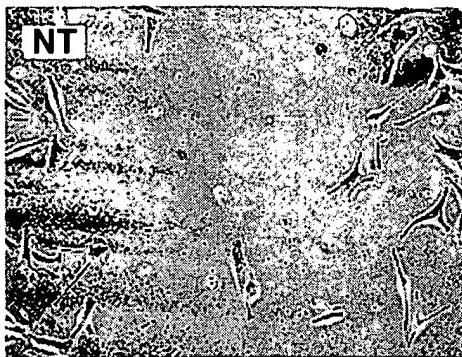


**FIG. 13C**

**FIG. 14A****FIG. 14B****FIG. 14C**

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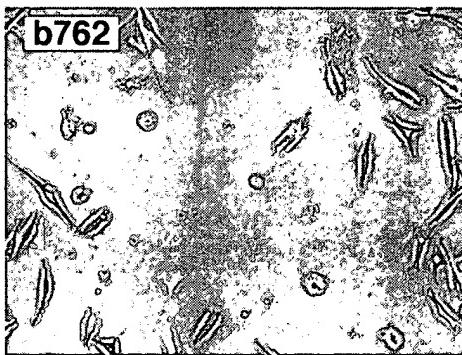
**FIG. 15**



**FIG. 16A**



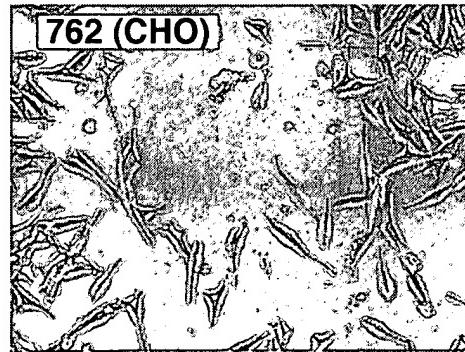
**FIG. 16C**



**FIG. 16B**

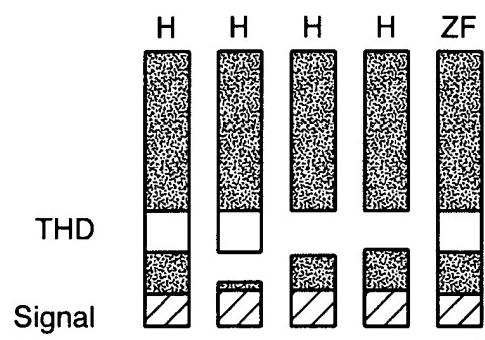


**FIG. 16D**

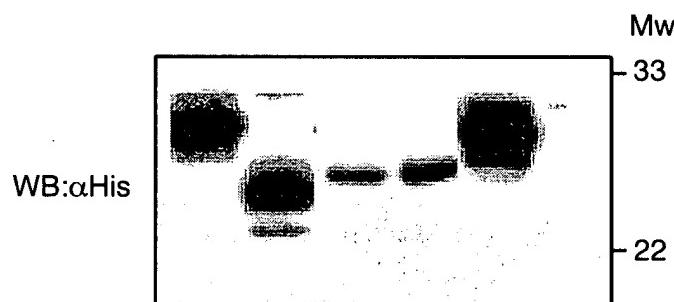


**FIG. 16E**

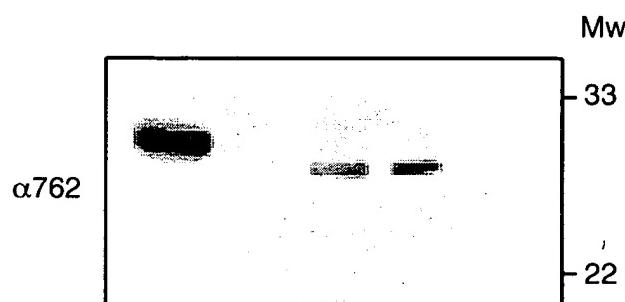
11 / 74



**FIG. 17A**



**FIG. 17B**



**FIG. 17C**

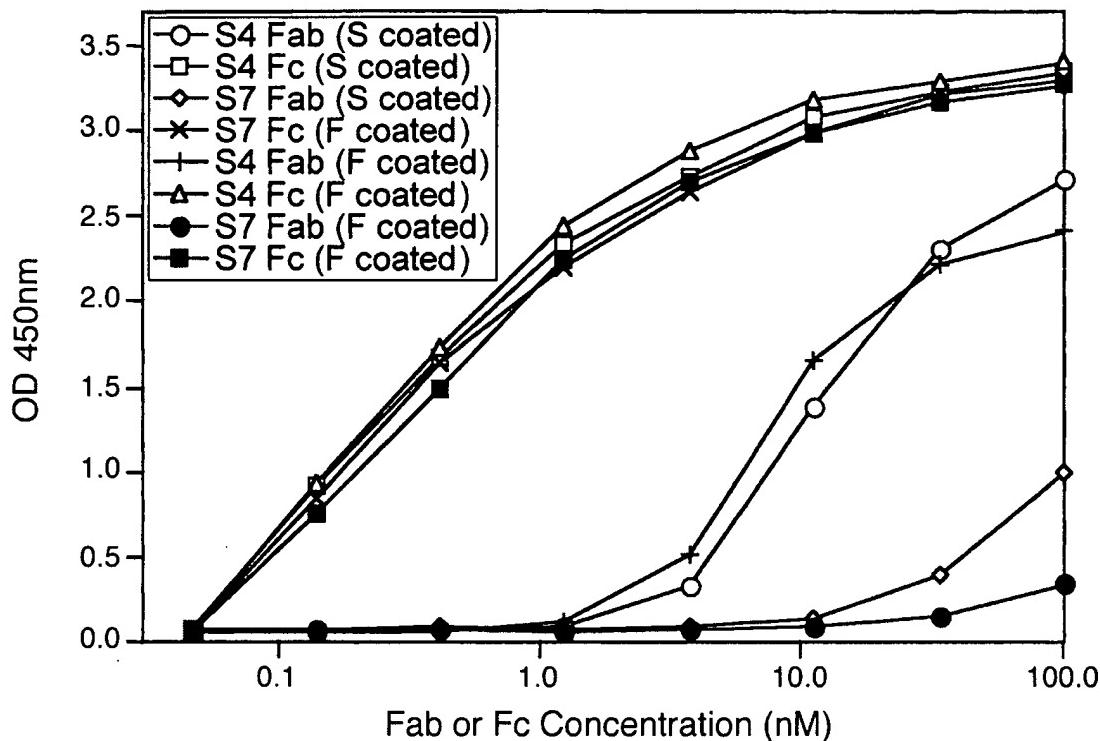
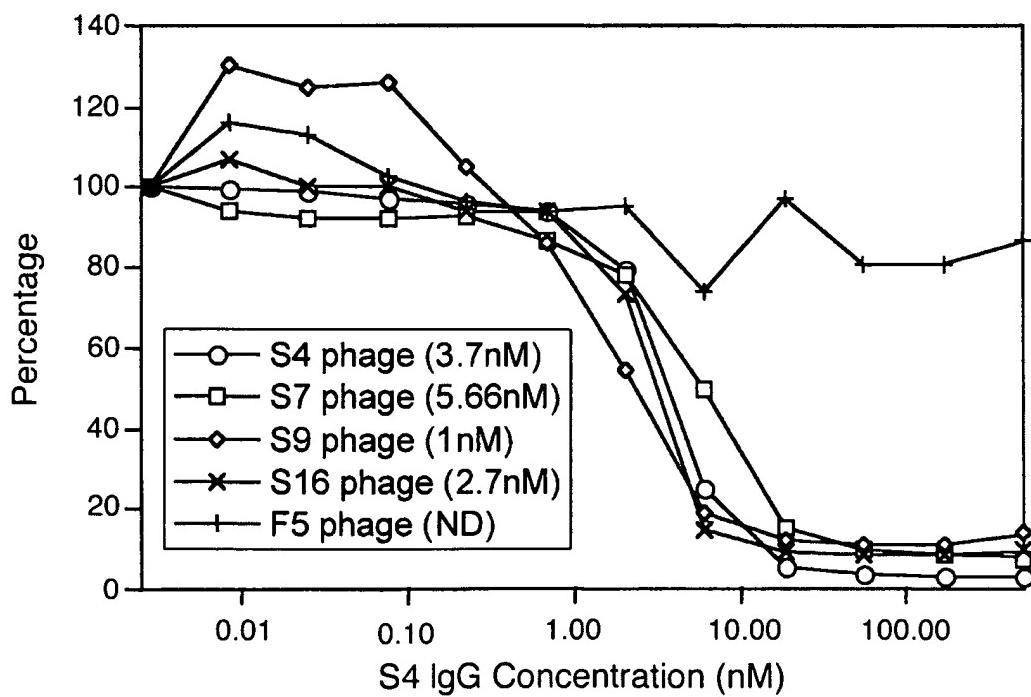
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H1			H2												H3																
28	29	30	31	32	33	49	50	51	52	52a	53	54	55	56	57	58	92	93	94	95	96	97	98	99	100	100a	100b	100c	101	102	Name
T	-	S	G	S	D	G	R	I	S	P	Y	G	G	N	T	N	C	A	R	V	G	L	K	L	L	-	F	D	Y		
T	-	T	N	S	D	A	T	I	Y	P	Y	G	G	Y	T	Y	C	A	R	G	G	M	D	G	Y	V	M	D	Y		
T	-	N	N	Y	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	
T	-	N	N	Y	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	
T	-	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	L	Y	W	V	-	F	D	Y		
T	-	S	N	Y	G	G	R	I	S	P	S	N	G	S	T	Y	C	A	K	C	S	V	R	-	-	-	F	A	Y		
T	-	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	
T	-	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	

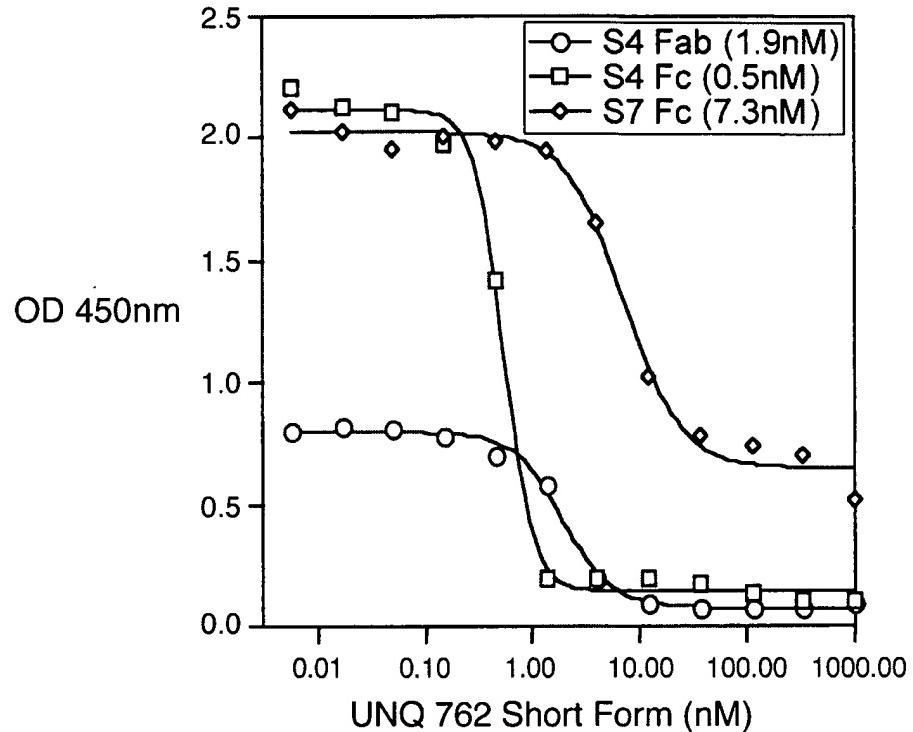
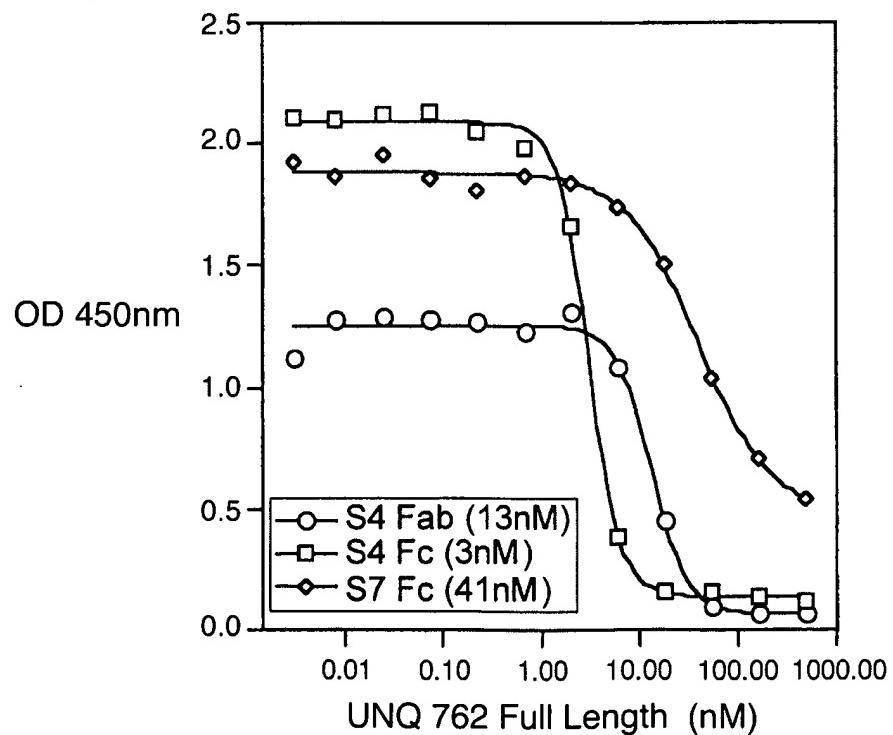
F/G. 18

Phage	Fab			IgG		
	762 S/S	762 F/F	762 S/S	762 F/S	762 F/F	762 S/S
S4	3nM	0.9nM	3.6nM (1.9nM)	32nM	13.4nM	0.5nM
762 S/S	762 F/F	762 S/S	762 F/S	762 F/F	762 S/S	762 F/F
S7	35nM	2.7nM	113nM	57nM	n/a	7.3nM

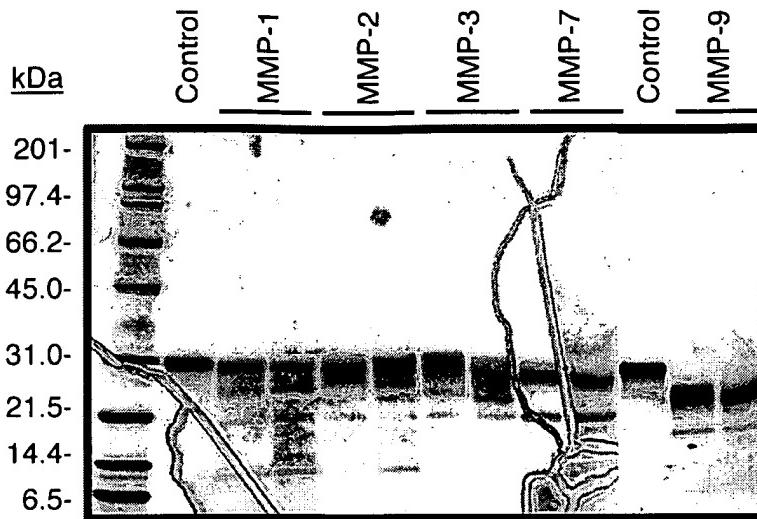
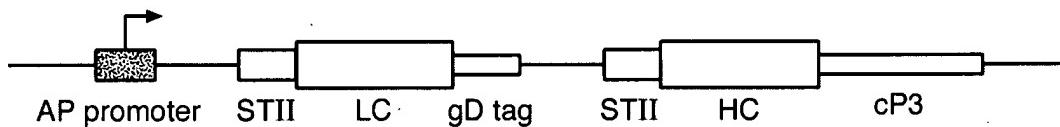
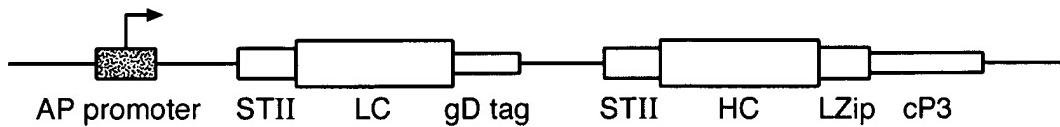
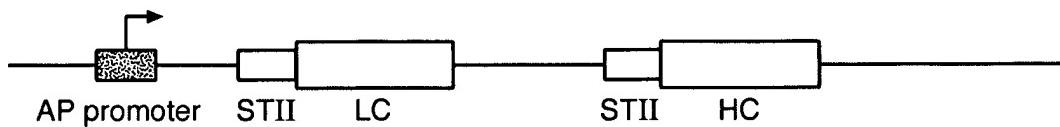
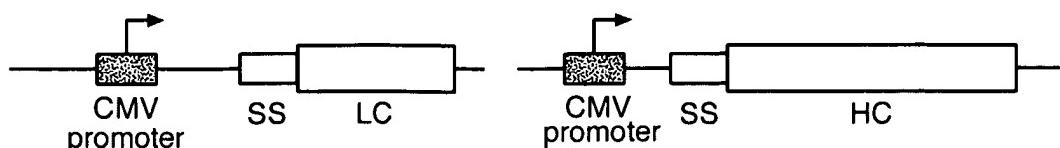
F/G. 21

**FIG. 19****FIG. 22**

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**FIG. 20A****FIG. 20B**

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**FIG. 23****FIG. 24A****FIG. 24B****FIG. 24C****FIG. 24D**

1 GAATTCAACT TCTCCATACT TGGATAAGG AAATACAGAC ATGAAAATC TCATTGCTGA GTTGTATT AAGCTTGCCC AAAAGAAGA AGAGTCGAAT  
CTTAAGTGA AGAGGTATGA AACCTATTC TTTATGCTG TACTTTAG AGAACGACT CAACATCAA TTCGAACGGG TTTTTCTCT TCTCAGCTTA  
CTTGACACAC GCGTCCATCT CGGAAACCTC TAATAGCAGT GACGTACGA AGCGTTATAC CGGGTTTAC CGGGTTAC TGGTGTGCC CAACTAACTA GTCCATCTCC

101 GAACTGTGTG CGCAGGTAGA AGCTTGGAG ATTATGCTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGGG GTTGTATGAT CAGGTAGAGG  
GGGGCTGTA CGAGGTAAG CCCGATGCCA GCATTCTGA CGACGATAACG GAGGTGCTGC GCGATTACGT AAAGAAGTAA TTGAAGCATC CTCGTCAGTA  
CCCGGCACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGAC CGCTATGCA TTCTCTCAAT AACCTCTGAG GAGCAGTCAT

201 AAAAGTTAAT CTTTCAAACA GCTGTATAA AGTTGTACAG GCCGAGACTT ATAGTCGCTT TGTTTTATT TTTAATGTA TTGTAACTA GTACGCAAGT  
TTTCAATTAA GAAAAGTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACACAAATAA AAAATTACAT AAACATGTAT CATGGTTCA

301 AAAAGTTAAT CTTTCAAACA GCTGTATAA AGTTGTACAG GCCGAGACTT ATAGTCGCTT TGTTTTATT TTTAATGTA TTGTAACTA GTACGCAAGT  
TTTCAATTAA GAAAAGTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACACAAATAA AAAATTACAT AAACATGTAT CATGGTTCA

401 TCACGTAAAA AGGGTATGTA GAGGTGAGG TGATTATTG AAAAGAATA TCGCATTCT TCTTGCATCT ATGTTGCTT TTCTTATGTC TACAAATGCC  
AGTGCATTT TCCCCATACAT CTCCAACCTC ACTAAATAAC TTTCCTTAT AGCGTAAAGA AGAACGTAGA TACAAGCAAA AAAGATAACG ATGTTACGG  
1 M K N I A F L L A S M F V F S I A T N A  
^start of stII signal sequence  
^met

501 TATGCAGATA TCCAGATGAC CCAAGTCCCCG AGCTCCCTGT CGGCCTCTGT GGGGATAGG GTCACCATCA CCTGCGGTGC CAGTCAGGAT GTGTCACACTG  
ATACGTCTAT AGGTCTACTG GGTCAAGGGC TCGAGGAGACA GGCGGAGACA CCCGCTATCC CAGTGGTAGT GTCAGTCTA CACAGGTGAC  
22 Y A D I Q M T Q S P S L S A S V G D R V T I T C R A S Q D V S T A  
^start of light chain  
^CDR-L1

601 CTGTAGCCTG GTATCAACAG AAACCAGGA AAGCTCGAA GCTCTCGATT TACTCGGAT CCTTCCTCTA CCTCTGGAGTC CCTCTCGCT TCTCTGGTAG  
GACATCGGAC CATACTGGTC TTGGTCTT TTGAGGCTT CGAAGACTAA ATGAGCGCTA GGAAGGAGAT GAGACCTAG GGAAGAGCGA AGAGACCATC  
56 V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S  
^CDR-L2

701 CGGTTCGGG AGGGATTCA CTCTGACCAT CAGGAGCTG CACCCGGAA ACTTCGCAAC TTATTACTGT CAGGAATCTT ATACTACTCC-TCCACAGTTC  
GCCAAGGGCC TGCCTAAAGT GAGACTGGTA GTCGTAGAC GTCGGCCTTC TGAAGCGGTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGGTGCAG  
89 G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F  
^CDR-L3

**FIG.\_25A**

801 CCAAGGGTA CCAAAACGA GATCAAACGA ACTGTGGCTG CACCATCTGT CTCATCTGT CGCCATCTC CGGCCATCTG ATGAGGAGTT GAAATCTGGA ACTGCCTCTG  
CCTGTCCTAT GGTTCCATT CTAGTGTGCT TGACACCGAC GTGGTAGACA GAAAGTAGAAC TACTCGTCAA CTTAGACCT TGACGGAGAC  
122 G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V

901 TTGTGTGCT GCTGAATAAC TTCTATCCA GAGAGGCCAA AGTACAGTGG AGGTTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTACAGA  
AACACACGGG CGACTTATG AAGATAGGGT CTCTCGGGT TCATGTACC TTCCACCTAT TGCGGGAGGT TAGCCCAATTG AGGGTCCCT AGGGTGTCT  
156 V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E

1001 GCAGGACAGG AAGGACAGCA CCTACAGCCT CAGGAGCAC CTGAGGCTGA GCAAAAGGAGA CTACGGAGAA CACAAAGTCT ACGCCCTGCGA AGTCACCCAT  
CGTCCTGTCG TTCTCTGCT GTGATGTCGA GTCGTCGTCG GACTGCACT CGTTICGCT GATGCTCTT GTGCTCTT GTGTTTCAGA TGCGGACGCT TCAGTGGTA  
189 Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H

1101 CAGGGCCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGATATGGCTG ATCCGAACCG TTTCGGGGT AAGGACCTGG  
GTCCCCGGACT CGAGGGGCA GTGTTCTCG AAGTGTCCC CTCTCACACC ACGGTCGAGG CCATACCGAC TAGGGCTGGC AAAGGGCCA TTCCGGACC  
222 Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L A

^ end of light chain, start of gd tag

1201 CATAACTCGA GGCTGATCCT CTACGCCGGA CGCATCGTGG CCCTAGTACG CAAGTTCACG TAAAAAGGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA  
GTTATTGAGCT CCGACTAGGA GATGCGGCCCT GCGTAGCACCC GGGATCATGC GTTCAAGTGC ATTTCCTCCA TTGATCTCCA ACTCCACTAA AATACTTTTT  
256 0

-23

M K K  
^ start of stII

1301 GAATATCGCA TTTCTCTTG CATCTATGTT CGTTTTCT ATTGCTACAA ACGGGTACGC TGAGGTTCA CGTGGTGGAGT CTGGGGTGG CCTGGTGCAG  
CTTATAGCGT AAAGAAGAAC GTAGATACAA GCAAAAAGA TAACATGTT TGGCATGCG ACTCCAAAGTC GACCCACCTCA GACCCACCTCA GGACACGTC  
-20 N I A F L L A S M F V F S I A T N A E V Q L V E S G G G L V Q

^ start of heavy chain

1401 CCAGGGGGCT CACTCGTTT GTCCCTGTGCA GCTTCTGGCT TCACATTTA AGACACCTAT ATACACTGGG TGCGGTCAAGGC CCCGGGTAAAG GGCGTGGAAAT  
GGTCCCCCGA GTGAGGCAA CAGGACACGT CGAAGACGA AGTTGTAATT TCTGTGGATA TATGTGACCC ACCGAGTCCG GGGCCATTG CCGGACCTTA  
14 P G G S L R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E W  
^CDR-H1

**FIG.\_25B**

1501 GGGTTGCAAG GATTATCCT ACGAATGGTT ATACTAGATA TGCCGATAGC GTCAAGGGCC GTTTCACCAT AAGGCCAGAC ACATCCAAA ACACAGCCTA  
 CCCAACGTC CTAATAGGA TGCTTACCAA TATGATCTATCG CAGGTCTATCG CAGTCCCCGG CAAAGTGATA TTTCGGCTCTG TGTAGGTTT TGTGTCGGAT  
 48 V A R I Y P T N G Y T R Y A D S V K G R F T I S A D T S K N T A Y  
 ^CDR-H2

1601 CCTACAAATG AACAGCTAA GAGCTGAGGA CACTGCGTC TATTATTGTA GCGGCTGGGG AGGGGACGGC TTCTATGCTA TGGACTACTG GGTCAAGGA  
 GGATGTTTAC TTGTGAAATT CTCGACTCT GTGACGGCAG ATAATAACAT CGGGCGACCC TCCCCTGCCG AAGATAACGAT ACCITGATGAC CCCAGTTCCCT  
 81 L Q M N S L R A E D T A V Y Y C S R W G D G F Y A M D Y W G Q G  
 ^CDR-H3

1701 ACACTAGTCA CGGTCTCC CCGCCTCCACC AAGGGCCAT CGGTCTCC CCGGGCACCC TCCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT  
 TGTGATCAGT GGCAGAGGG CCGGAGGG CCAGGAGGG TTCCCGGGTA GCAGAAGGG GGACCGTGGGG AGGGGGTCT CGTGGAGAAC CCCGGTGTGC CGGGACCCGA  
 114 T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C

1801 GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTGTC GTGGAACACTCA GGCGCCCTGA CCAGGGGGGT GCACACCTTC CCGGCTGTCC TACAGTCTC  
 CGGACCAAGTT CCTGATGAAG GGGCTTGGCC ACTGCAACAG CACCTTGAGT CCGCGGGACT GGTCGGCGCA CGTGTGAAAG GGCCGACAGG ATGTCAGGAG  
 148 L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S  
 ^end of heavy chain

1901 AGGACTCTAC TCCCTCAGCA GGGGGTGAC CGTGCCCTCC AGCAGCTTC GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCAG CAACACCAAG  
 TCCTGAGATG AGGGAGTCGT CGCACCACTG GCACGGGAGG TGTGCAACC CGTGGTCTG GATGTAGACGC TTGACTTAG TGTTGGGTG GTGTTGGTTC  
 181 G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K  
 ^start of gene III coat protein (267-end)

2001 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAACTC ACTCTAGTGG CGGTGGCTCT GTTTCGGTG ATTTGATTA TGAAAGATG GCAAACGCTA  
 CAGCTGTTCT TTCAACTCGG GTTTAGAACCA CTGTTTGAG TGAGTCACC GCCACCGAGA CCAAGGCCAC TAAAACATAAT ACTTTCTAC CGTTGGGAT  
 214 V D K K V E P K S C D K T H L S G G S G D F D Y E K M A N A N  
 ^end of heavy chain

2101 ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGGCT ACAGTCTGAC GCTAAAGGCA AACTGATTG TGTCGCTACT GATTACGGTG CTGCTATCGA  
 TATTCCCCCG ATACTGGCTT TTACGGCTAC TTTCGGCTT TTGAGACTG CGATTCCGT TTGAGACTAAG ACAGCGATGA CTAATGCCAC GACGATAGCT  
 248 K G A M T E N A D E N A L Q S D A K G K L D S V A T D Y G A A I D

**FIG.\_25C**

2201 TGGTTTCATT GGTGACGTTT CCGGCCCTTGC TAATGGTAAT GGTGCTACTG GTGATTTCGC TGGCTCTAAT TCCCAAATGG CTCAAGTCGG TGACGGTGT  
 ACCAAAGTAA CCACTGCAA GGCGGAAACG ATTACCATTA CCACGATGAC CACTAAACG ACCGAGATA AGGGTTAACCG TTGTTAGCAGCC ACTGCCACTA  
 281 G F I G D V S G L A N G N G A T G D F A G S N S Q M A Q V G D G D

2301 ATTCACTT TAATGAAATA TTTCGGTCAA TATTIACCTT CCCTCCCTCA ATCGGTGMA TGTGGTCTTAA TTGCTCTTAG CGCTGGTAAA CCATATGAAAT  
 TAAAGTGAA ATTACTTAAAGGCAATT ATAAATGGAA GGAGGGAGT TAGCCAACTT ACAGGGAA AACAGAAATC GCGACCAATT GGATACTTA

314 N S P L M N N F R Q Y L P S L P Q S V E C R P F V F S A G K P Y E F

2401 TTCTATGAA TAAACTTAT TCCGTGGTGT CTGGCGTTT CTTTATATG TTGGCACCTT TATGTATGTT TTTCTACGT TTGCTAACAT  
 AAAGATAACT AACACTGTT TATTGAAATA AGGCACCAAA GAAACGCAA AAAATATAC AACGTTGAA ATACATACAT AAAAGATGCA AACGATTGTA

348 S I D C D K I N L F R G V F A F L L Y V A T F M Y V F S T F A N I

2501 ACTGGTAAT AGGAGCTT AATCATGCCA GTTCTTTGG CTAGGCCGC CCTATACTT GTCTGCCTCC CGCGCTTGGC TCGGGTGCAG TGAGCCGGG  
 TGACGCCATT TTCTAGAA TTAGTAGGT CAAGAAAACC GATCGGGCG GGATATGAA CAGACGGGG GGCACAAACGC AGGCCACGT ACTCGGGCC

381 L R N K E S O

2601 CCACCTCGAC CTGAATGGAA GCCGGCGGCA CCTCGTAAC GGATTCAAC CTCCAAGAAT TGGAGCCAAT CAATTCTTGC GGAGAACTGT GAATGCGCAA  
 GGTGGAGCTG GACTTACCTT CGGGCGGGT GGAGGATTT CCTAAGTGGT GAGGTTCTTA ACCTCGGTTA GTTAAGAACG CCTCTTGACA CTACGCGTT

2701 ACCAACCTT GGAGAACAT ATCCATCGCG TCCGCATCT CCAGCAGCCG CACGGGGCG ATCTCGGGCA GCGTTGGGT CTGGGCCACGG GTGCGCATGA  
 TGGTGGAA CGCTCTGTA TAGGTAGGCC AGGGGTAGA GTGCGCTGGC GTGCGCCGG TAGMCCCCGT CGCAACCCAG GACCGGTGCC CACGGTACT

2801 TCGTGCCTT GTCGCTGAGG ACCGGGTAG GCTGGGGGG TTGCTCTACT GGTAGGAGA ATGAAATCACC GATACGGAG CGAACGTGAA CGGACTGCTG  
 AGCACGGGA CAGCAACTCC TGGCGCATC CGACCGCCCC AACGGAATGA CCAATGCTT TACTTAGTGG CTATGCGCTC GCTTGACTT CGCTGACGAC

2901 CTGCAAACG TCTGGACCT GAGCAACAAAC ATGAATGGTC TTGGTTTCC GTGTTCTGTA AAGTCTGGAA ACGGGAAAGT CAGGGCCCTG CACCATATTG  
 GACGTTTGC AGACGCTGAA CTGCGTGGC AGACGACAC CTCGTTGTTG TACTTACCG AAGCCAAAGG CACAAAGCAT TTCAAGACCTT TGCGCCCTCA GTGGTAATAAC

3001 TTCCGGATCT GCATCGCAGG ATGCTGCTGG CTACCCCTGTTG GACACCTAC ATCTGTATTAAACGAGGCTT GGGATTGACCT GCGGTTCTGGT  
 AAGGCCTAGA CGTAGGGTCC TAGGACGACAC CTGTTGGATG TAGACATTAAT TGCTTCGGGA CGGTAACCTGG GACTCACTAA AAAGAGACCA

3101 CCCGCCGAT CCTACCGCC AGTTGTTCAC CCTCACAAACG TTCCAGTAAC CGGGCATGTT CATCATCAGT AACCCGTATC GTGAGCATCC TCTCTCGTT  
 GGGGGCGTA GGATGGGG TCAACAAATG GGAGTGTGC AAGGTCTTG GCCGTACTA GTAGTAGTCA TTGGGCATAG CACTCGTAGG AGAGAGAAA  
  
 3201 CATGGTATC ATTACCCCA TGAACAGAAA TTCCCCCTTA CACGGGCA TCAAGTGCAC AAACAGGAA AACCCGCCCT TAACATGCC CGCTTATCA  
 GTAGCCATAG TAATGGGGT ACTTGTCTTT AAGGGGAAT GTGCTCCGT ATGTCACTGG TTGTCTCTT TTGGGGGA ATFTGACCG GCGAAATAGT  
  
 3301 GAAGCCAGAC ATTAACGCTT CTGGAGAAC TCAACGAGCT GGACGGGAT GAACAGGGAG ACATCTGTGA ATCGCTTCAC GACCACGCTG ATGAGCTTA  
 CTTCGGTCTG TAATGGCAA GACCTCTTGG AGTTGCTGA CCTGGCCTA CCTGGTCCGGT TGTAACACT TAGCGAAGTGT CGGTGCGAC TACTCGAAAT  
  
 3401 CGCGAGATC CGGAAATTGT AAACGTTAAT ATTTTGTAA AATTGCGTT AAATTTTGT TAAATCAGT CATTTTTAA CCAATAGGCC GAAATCGGCA  
 GGGGTCTAG GCCTTTAACAA TTGCAATT TAAACATT TTAGGCCAA TTAAACAA ATTAGTCGA GTAAAAAAATT GTTATCCGG CTTAGCCGT  
  
 3501 AAATCCCTTA TAAATCAAA GAATAGACCG AGATAGGGTT GAGTTGTGC CAGTTGGCA ACAACAGTCC ACTATTAAG AACGTGGACT CCAACGTCAA  
 TTAGGGAAAT ATTAGTTT CTATCTGGC TCTATCCAA CTCACAACAA GTCAAAACCT TGTTCTCAGG TGATAATTTC TTGACCTGA GTTGCAGTT  
  
 3601 AGGGGAAA ACCGCTCTATC AGGGCTATGG CCCACTACGT GAACCATCAC CTAATCAAG TTTTGGGG TCGAGGTGCC GTAAAGGACT AAATGGAAC  
 TCCCCTCTTT TGGCAGATAG TCCCGATACC GGGTGATGCA CTTGTAAGTGC GGATTAGTC AAAAACCCC AGCTCCACGG CATTTCGTGA TTAGCCTG  
  
 3701 CCTAAAGGA GCCCCGGATT TAGAGCTTGA CGGGAAAGC CGGGAACGT GGCAGAAAGG GAAGCCAGAAGG AAGCGAAAGG AGCGGGGCT AGGGCGCTGG  
 GGATTCCCT CGGGGGCTAA ATCTGAACCT GCCCCTTGCG CCGCTGCA CGCTCTTCTC TTGCGTTTCC TCGCCCGGA TCCCGGACCC  
  
 3801 CAAGTGTAGC GGTCACTGCGT CGGGTAACCA CCACACCGC CGCTTAAT GGGGGCGTAC AGGGGGCTC CGGATCCCTGC CTCGCGCGTT CGGGTGTGA  
 GTTCACTCG CCAGTGCAC GGGCATGGT GGGGAATT CGGGGGATG TCCCGGCAG GCCTAGGACG GAGCGGCAA AGCCACTACT  
  
 3901 CGGTGAAAC CTCTGACACA TGGAGCTCCC GGAGACGGTC ACAGCTGTC TGTAAGGGA TGCCGGGAGC AGACAAGCCC GTCAAGGGC GTCAAGGGGT  
 GCCACTTTG GAGACTGTG ACGTGAGGG CCTCTGCGAG ACATTCGCTCG TGTGAACAG ACATTCGCTCG TCTGTTGGG CAGTCCCG CAGTCGCCCA  
  
 4001 GTTGGGGGT GTGGGGGGC AGCCATGACC CAGTCACGTA GGGATAGGG AGTGTATACT GGCTTMACTA TGGGGCATCA GAGGAGATG TACTGAGGT  
 CAACCGCCCA CAGCCCCGGC TCGGTACTGG GTCACTGCAT CGCTATGCC TCACATATGA CGGAATTGAT ACCGGCGTAGT CTCGCTAAC ATGACTCTCA

4101 GCACCATATG CGGTGTGAAA TACCGCACAG ATGGTAAGG AGAAAATACC GCATCAGGGCG CTCCTCCGCT TCCTCGCTCA CTGACTCGT GGCCTCGTC  
CGTGGTATAC GCCACACTT ATGGGTGTC TAGCATTCC TCTTTATCC CGTAGTCGCC GAGAAGGGCA AGGGCGAGT GACTGACCGA CGGAGCCAG

4201 GTTCGGCTGC GGGAGGGT ATCAGCTAC TCAAAGGGGG TAATAACGGT ATCCACAGAA TCAGGGGATA ACAGAGAAA GAACATGTGA GCAAAAGGCC  
CAAGCCGACG CCGCTGCCA TAGTCGAGTG AGTTCCGCC ATTATGCCAA TAGGCCAA TAGGTGTCTT AGTCCCCAT TGCGTCCTT CTGTCACACT CGTTTCCGG

4301 AGCAAAAGGC CAGGAACCGT AAAAAGGCC CGTTGCTGGC GTTTTCCAT AGGTCGGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG  
TCGTTTTCGG GTCCTGGCA TTTCGGC GCAACGACG CAAAGGTA TCCGAGGGG GGGGACTGCT CGTAGTGTCTT TTAGCTGGCA GTTCAGTCCTC

4401 GTGGCGAAC CGCACAGGAC TATAAGATA CCAGCGTTT CCCCTGGAA GCTCCCTCGT GCGCTCTCCGT GTTCCGACCC TGCCGTTAC CGGATACCTC  
CACCGCTTTG GGCCTCCTG ATATTCTAT GGTCCGCAAA GGGGGACCTT CGAGGGAGCA CGGGAGAGGA CAAGGCTGGG ACGGGAAATG GCTATGGAC

4501 TCCGCCCTTC TCCCTCGGG AAGCGTGGC CTTCTCATA GCTCACGGCTG TAGGTATCTC AGITCGGTGT AGITCGTTG CTCCAAGCTG CTCCAGCTG  
AGGGGAAAG AGGGAAAGCCC TTGGCACCGC GAAAGAGTAT CGAGTCGAC ATCCATAGAG TCAAGGCCACA TCCAGCAAGC GAGGTGTCGAC CGACACACG

4601 ACGAACCCCC CGTCAGGCC GACCGCTGG CCTTATCCGG TAACTATCGT CTTGACTCCA ACCCGGTAAAG ACACGACTTA TGGCCACTGG CAGCAGCCAC  
TGCTTGGGG GCAAGTGGG CTGGCACGC GGAATAGGCC ATGATAGCA GAACTCAGGT TGGCCATTCT TGTCGTGAAT AGGGGTGACCG GTCGTCGGT

4701 TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGGGTGCT ACAGAGTTCT TGAAGTGGT GCTTAACTAC GGCTAACATA GAAGGACAGT ATTGGTATC  
ACCATGTC TAAATGTC GCTCCATACA TCCGCACGA TGCTCAAGA ACTTCACCCAC CGGATTGATG CCGATGTGAT CTTCCGTCA TAAACCATAG

4801 TGGGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG GTAGCTCTG ATCCGGCAA CAAACACCG CTGGTAGGG TGTTTTTT GTTGCAAGC  
ACGGGAAGCG ACTCGGTCA ATGGAAGCT TTTCTCAAC CATCGAGAAC TAGGCCGTT GTTGGTGGC GACCATGCC ACCAAAAAA CAAACGTTCG

4901 AGCAGATTAC GGGAGAAAA AAAGGATCTC AGAAGATCC TTGATCTT TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATT  
TCGTCATATG CGCGTCTTT TTCCCTAGAG TTCTCTAGG AACTAGAAA AGATGCCAA GACTGCGAGT CACCTTGCTT TTGAGTGCAA TTCCCTAAA

5001 GGTCAATGAGA TTATCAAAA GGATCTCAC CTAGATCCTT TAAAGTATAT ATGAGAAGTT TAAATCAATC GTGAGTAAAC TTGGTCTGAC  
CCAGTACTCT AATAGTTTT CCTAGAAGTG GATCTAGGA AATTAATT TTACTCTAA ATTACTATAG ATTCTATATA TACTCATATA TACTCATATA TACTCATATA

5101 AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTAAGCGA TCGTGTCAATT TCGTGTCAATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC  
 TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGACTCGCT AGACAGATAA AGCAAGATAA TATCAACGGA CTGAGGGCA GCACATCTAT TGATGCTATG  
  
 5201 GGGAGGGCTT ACCATCTGGC CCCAGTGTG CAATGATAACC GCGAGACCCA CGCTCACCGG CTCCAGATT ATCAGCAATA AACCAGCCAG CGGAAGGGC  
 CCCTCCCGAA TGGTAGACCG GGGTACCGAC GTTACTATGG CGCTCTGGGT GCGAGTGGCC GAGGTCTAA TAGTCGTAT TTGGTGGTC GGCTTCCC  
  
 5301 CGAGGCCAGA AGTGGTCTGC CAACTTTATC CGCCTCCATC CAGTCATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGCGC  
 GCTCGGTCT TCACCAAGAC GTTGAAATAG GCGGAGGTAG GTCAAGATAAT TAACAACGGC CCTTCGATCT CATTCAAA GGGTCATT ATCAAACGGC  
  
 5401 AACGTTGTTG CCATTGCTGC AGGCATCGT GTGTOACCGT CGTCGTTTG TATGGCTTCA TTCAAGCTCCG GTTCCCAACG ATCAAGGCAGA GTTACATGAT  
 TTGCAACAAC GGTAAACGAG TCCGTAGCAC CACACTGGCA CGAGCAAAAC ATACCGAAAGT AAGTCGAGGC CAAGGGTGC TAGTTCGGCT CAATGACTA  
  
 5501 CCCCATGTT GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAAGAAGTA AGTCAGAAGTC AGTGGTTACA CTCATGGTTA TGGCAGGACT  
 GGGGGTACAA CACGTTTTT CGCCAAATGCA GGAAGCCAGG AGGCTAGCAA CAGTCCTCAT TCAACCGGGC TCACAATAGT GAGTACCAAT ACCGTCGTGA  
  
 5601 GCATAATTCT CTTACTGTCA TGCCATCGT AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGGC GCGACCCGAGT  
 CGTATTAAAGA GAATGACAGT ACGGTAGCA TTCTACGAA AGACACTGAC CACTCATGAG TTGGTTCACT AAGACTCTA TCACATACGC CGCTGGCTCA  
  
 5701 TGCTCTGCC CGGGTCAAC ACGGGATAAT ACCGGCCAC ATAGCAGAAC TTAAAAGTG CTCACTCATG GAAAACGTC TTGGGGCGA AAACTCTCAA  
 ACAGGAACGG GCGCACTG TGCCCTATA TGGCCTG TATCGTCTTG AAATTTCAC GAGTAGTAAC CTTTGCAAG AAGCCCGCT TTGAGAGT  
  
 5801 GGATCTTACG GCTGTTGAGA TCCAGTTCGA TGTAAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTT TACTTCACC AGCGTTCTG GGTGAGCAA  
 CCTAGAATGG CGACAACCT AGGTCAAGCT ACATTGGTG AGCACCTGGG TTGACTAGAA GTCGTAGAAA ATGAAAGTGG TGCAAGAC CCACTCGTT  
  
 5901 AACAGGAAGG CAAATGCCG GTTTTACGGC GTTTTACGGC TTATTCCGC TTGTCCTTA CAACTATGA GTATGAGAAG GAAAAGTAA TAATAACTTC GAAATAGTC  
  
 6001 GGTTATGTC TCATGAGGG ATACATATT GAATGTTATT AGAAAATAA ACAAAATAA GAAATAGGG GTTCGGCGCA CATTTCGGCA AAAAGTGGCA CCTGACGGTCT  
 CCAATAACAG AGTACTCGCC TATGTTAAA CTTACATAAA TCTTTTTATT TGTTTACCC CAAGGGCGT GTAAAGGGC TTTTACCGT GEACTGGCAGA

**FIG. - 25G**

6101 AAGAACCCT TATTATCATG ACATTAACCT ATAAAATAG GCGTATCACG AGGCCCTTTC GTCCTCAATA CAGGTAGACC TTTCGTAGAG ATGTACAGTG  
 TTCTTTGGTA ATAATAGTAC TGTAATTGGA TATTTTATC CGCATAGTGC TCCGGAAAG CAGAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTCAC  
  
 6201 AAATCCCGA AATTATACAC ATGACTGAAG GAAGGGACT CGTCATTCCC TGGCGGTAA CGTCACCTAA CATCACTGTT ACTTTAAAAA AGTTCCACT  
 TTAGGGCT TAAATATGTG TACTGACTTC CTTCCTCGA GCAGTAAGGG AGGGCCCAAT GCAGTGGATT GTAGTGACAA TGAATTTT TCAAAGGTGA  
  
 6301 TGCACCTTG ATCCCTGATG GAAAACCGAT AATCTGGAC AGTAGAAAGG GCTTCATCAT ATCAATGCA ACGTACAAG AAATAGGGCT TCTGACCTGT  
 ACTCTGAAAC TAGGGACTAC CTTTGCGTA TTAGACCTG TCACCTTCC CGAACCTGA TAGTTACGT TGACATGTTIC TTATCCGA AGACTGGACA  
  
 6401 GAGGCAACAG TCAATGGCA TTGTATAAG ACAAAACTAC TCACACATCG ACAAACCAAT ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGGAAAT  
 CTTCGTTGTC AGTACCCGT AAACATATTTC TGTTGATAG AGTGTGAGC TGTTTGGTTA TGTTATGTC ATCTGGAAG CATCTCACA TGTCACTTAA  
  
 6501 CCCCGAAATT ATACACATGA CTGAAGGAAG GGAGCTGTC ATTCCTGCC GGGTTACGTC ACCTAACATC ACTGTTACTT TAAAAAGTT TCCACTTGAC  
 GGGGCTTAA TATGTTACT GACTTCCTTC CCTCGACAG TAAGGGACGG CCCATGCG AGTGGATGTAG TGACAATGAA ATTTTCAA AGGTGAACTC  
  
 6601 ACTTGATCC CTGATGGAA ACCGATAATC TGGGACAGTA GAAAGGGCTT CATCATATCA AATGCAACGT ACAAAAGAAAT AGGGCTTCTG ACCTGTGAAG  
 TGAAACTTGG GACTACCTTT TGCGTATTAG ACCCTGTCACTT CTTCCGAA GTAGTATACTT TTACGTGCA TGGTCTTTA TCCCGAAGAC TGGACACTTC  
  
 6701 CAACAGTCAA TGGCATTG TATAAGACAA ACTATCTCAC ACATGACAA ACCAATACAA TCTACAGGT GACCTTTCGT AGAGATGTAC AGTGAATCC  
 GTTGTCAAGTT ACCCGAAAC ATATTCTGTT TGATAGTGT TGTAGCTGTT TGGTTATGTT AGATGTCCAT CTGGAAAAGCA TCTCTACATG TCACCTTAAAG  
  
 6801 CCGAAATTAT ACACATGACT GAAGGAAGGG AGCTCGTCAT TCCCTGCCGG GTTACGTCACTCAC TGTACTTTA AAAAGTTT CACTGACAC  
 GGCTTTAAATA TGTGTACTGA CTTCCTTCCC TCGAGGACTA AGGGACGGCC CAATGCGTG GATTGTAGTG ACAATGAAAT TTTTCAAAG GTGAACGTG  
  
 6901 TTGATCCCT GATGGAAAAC GCATAATCTG GGACAGTAGA AAGGGCTICA TCAATACAA TGCAACGTAC AAAGAAATAG GGCTTCTGAC CTGTGAAGCA  
 AAACTAGGGCA CTACCTTTG CGTATTAGAC CCTGTCACT TTCCGAAGT AGTATAGTT ACGTGGCATG TTCTTTATC CGGAAGACTG GACACTTCGT  
  
 7001 ACAGTCAATG GGCATTTGTA TAAGACAAAC TATCTCACAC ATGACAAAC GAAACATC  
 TGTCACTTAC CCGTAAACAT ATTCTGTTG ATAGAGTGTG TAGCTGTTG GTTATGTTAG

**F/G. - 25H**

1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTATT AAGCTTGGCC AAAAGAAGA AGAGTCGAAT  
CTTAAGTGTGA AGAGGTATGA AACCTATCC TTATGCTG TACTTTAG AGTAACGACT CACAATAAA TTGCAACGGG TTTTCTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATGCTCA CTGCAATGCT TC GGCAATATG GCGCAAAATG ACCAACAGGC GTTGATTGAT CAGGTAGAGG  
CTTGACACAC GCCTCCATCT TCGAAACCTC TAATAGCAGT GACGTACCA AGCGTATAC CGGGTTTAC CGGTGTTGC CAACTAACTA GTCCTCATCTC

201 GGGCGGTGTA CGAGGTAAG CCCGATGCCA GCATCCTGA CGACGATACG GAGCTGCTGC GGCGATTACGT AAAGAAGTT TTGAGCATC CTCGTCAGTA  
CCCCGGACAT GCTCCATTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTGACGACG CGGTAATGCA TTCTTCATAA AACTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTCAACA GCTGTCAAA AGTTGTCAAG GCCGAGACTT ATAGTCGCTT TGTTTAATGTA TTTGTAACTA GTACGCAAGT  
TTTCAATTAA GAAAAGTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAATAA AAAACATTACAT AAACATTGAT CATGCGTTCA

401 TCACGGAAA AGGGTATGTA GAGGGTGGG TGATTTATG AAAAGAATA TCGCAATTCT TCTTGCAATCT ATGTTGGTTT TTTCATTGC TACAAATGCG  
AGTGCATTT TCCCATACAT CTCCAACCTC ACTAAATAAC TTTTCTTAT AGCGTAAAGA AGAACGCTGAA TACAAGCAA AAAGATAACG ATGTTAACGG

1 M K N I A F L L A S M F V F S I A T N A  
^ start of stII sequence

501 TATGCATCCG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCGGCCTC TGTCGGCGAT AGGGTCACCA TCACCTGGCC TGCCAGTCAG GATGTTGCCA  
ATACGTGGC TATAGGTCTA CTGGGTCAAGG GGCTCGAGG ACAGGGGAG ACACCCGCTA TCCCACTGGT AGTGGACGGC ACGGTCAGTC CTACACAGGT  
22 Y A S D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T  
^ light chain start

601 CTGCTGTAGC CTGGTATCAA CAGAACCAG GAAAGCTCC GAAGCTCGG ATTTACTCGG CATCCCTTCCT CTACTCTGG GTTCTCTCTC GCTTCTCTGG  
GACGACATCG GACCATAGT GTCTTGTGTC CTTTCGAGG CTTCGAAGAC TAATAGGCC GTAGGAAGGA GATGAGACCT CAGGGAAAGAG CGAAGAGACC  
56 A V A W Y Q Q K P G K A P K L I Y S A S F L Y S G V P S R F S G  
^ CDR-L2

701 TAGGGTTCG GGGACGGATT TCACCTGAC CATCAGGACT CTGGCAGCCGG AACACTTCGG AACATTATTAC TGTCAGGAAT CTTTACTAC TCCTCCACG  
ATCGCCAAGG CCCTGCCTAA AGTGAAGCT GTAGTCGTC GACGTGGCC TTCTGAAGCG TTGAAATAATG ACAGTCGTTA GAATATGAGGGTGC  
89 S G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T  
^ CDR-L3

**F/G.-26A**

801 TTCGGACAGG GTACCAAGGT GGAGATCAA CGAACTGTGG CTGCACCACAT TTGCTTCATC TTGATGCCAT CTGATGAGCA GTTGAANACT GGAACCTGCC  
AAGCCGTGTC CAGGGTCCA CCTCTAGTT GCTTGACACC GACGTGGTAG ACAGAAGTAG AAGGGGGTA GACTACTGT CAACTTGA CCGTGACGGA  
122 F G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S

901 CTGTTGTGTG CCTGCTGAAT AACCTCTATC CCAGAGAGGC CAAACTACAG TGGAAGGTGG ATAACGCCCT CCATCGGGT AACTCCAGG AGAGTGTAC  
GACAACACAC GGACGACTTA TTGAGATAG GGTTCTCTCG GTTTCATGTC ACCTTCCAC TATTGGGGA GGTAGCCCC TTGAGGGTCC TCTCACAGTG  
156 V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T

1001 AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCACCCAG ACCCTGACGC TGAGCAAAGC AGACTACGG AGAACACAAAG TCTACGCCG CGAAGTCACC  
TCTCGTCCTG TCCTCTGT CGTGGATGTC GGAGTCGTG TGGAAGTGG ACTCGTTCTG TCTGATGCTC TTGTTGTTT AGATGGGAC GCTTCAGTGG  
189 E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T

1101 CATCAGGGCC TGAGCTGCC CGTCACAAAG AGCTTCACAA GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CGTTTCCGC GGTAAGGACC  
GTAGTCCGG ACTCGAGCCG GCAGTGTTC TCGAAGTTGT CCCCTCTCAC ACCACGGTCG AGGCCATACCC GACTAGGCTT GCAAAGGGC CCATTCTGG  
222 H Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L

^end of light chain, start of gd tag

1201 TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGGCATCG TGGCCCTAGT ACGCAAGTTC ACGTAAAAAG GGTAACTAGA GGTGAGGTG ATTATATGAA  
ACCGTATTGA GCTCCGACTA GGAGATGCC CCTGGTAC ACCGGATICA TGGGTCAAG TGCATTITTC CCATTTGACTT CCAACTCCAC TAATAACTT  
256 A O

-23  
-23

M K  
^start of stII

1301 AAAGAATATC GCATTTCTTC TTGATCTAT GTTCGTTT TCTATGCTA CAAACGGTA CGCTGAGGT CAGCTGGTG AGTCTGGGG TGGCTGGTG  
TTCCTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTGTGGCAT GCGACTCCAA GTGACCCACC TCAGACCC ACCGGACAC  
-21 K N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G G L V

^start of heavy chain

1401 CAGCCAGGG GCTCACTCCG TTTGCTCTGT GCAGCTTCG GCTTCACAT TAAAGACAC TATATACACT GGGTGGTCA GGGCCGGGT AAGGGCTGG  
GTCGGTCCCC CGAGTGGGG AACAGGACA CGTCGAAGAC CGAAGTGTGA ATATATGTGA CCCACGGCAGT CGGGGGCA TTCCGGACC  
13 Q P G G S L R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E

^CDR-H1

**FIG.-26B**

1501 AATGGCTTGC AAGGATTTAT CCTACGAATG GTTAATACTAG ATATGCCGAT ACCGTCAGG GCGTTTCAC TATAAGGCCA GACACATCCA AAAACACAGC  
 TTACCCAAACG TTCCCTAAATA GGATGCTAC CAATATGATC TATACGGCT TCGCAGTCC CGGAAAGTG ATATTCGGGT CTGTTAGGT TTTGTGTCG  
 47 W V A R I Y P T N G Y T R D S V K G R F T I S A D T S K N T A  
 ^CDR-H2

1601 CTACCTACAA ATGAAACAGCT TAAGAGGTGA GGACACTGCC GTCTTATTAT GTAGCCGCTG CCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGCACA GCGGCCCTGG  
 GATGGATGTT TACTCTGTCGA ATTCTGACT CCTGTGACGG CAGATAATA CATGGGAC CCCCTCCCTG CCGAAGATAAC GATACTGTAG GACCCCAAGT  
 80 Y L Q M N S L R A E D T A V Y Y C S R W G G D G F Y A M D Y W G Q  
 ^CDR-H3

1701 GGAACACTAG TCACCGCTTC CTCGGGCC ACCAAGGGCC CATCGGTCTT CCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGCACA GCGGCCCTGG  
 CCTTGTGATC AGTGGCAGAG GAGCCGGAGG TGGTTCGGG GTAGCCAGAA GGGGACCCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGAC  
 113 G T L V T V S A S T K G P S V F P L A P S S K S T S G G T A A L G

1801 GCTGCCCTGGT CAAGGACTAC TTCCCCAAC CGGTGACGGT GTCGTGGAAC TCAGGGCCC TGACCAGGG CGTGCACACC TTCCCGGTG TCCTACAGTC  
 CGACGGACCA GTTCCCTGATG AAGGGGCTTG GCCACTGCCA CAGCACCTTG AGTCCGGGG ACTGGTGCAC GCACCGTGG AAGGGCCGAC AGGATGTCG  
 147 C L V K D Y F P V T V S W N S G A L T S G V H T F P A V L Q S  
 ^CDR-H3

1901 CTCAAGGACTC TACTCCCTCA GCAGCGTGGT GACCGGTGCC TCCAGGAGT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAAGCC CAGCAACAC  
 GAGTCTGAG ATGAGGGAGT CGTGGCACCA CTAGGAGG AGGTCTGTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTGG GTCGTTGG  
 180 S G L Y S L S S V V T V P S S L G T Q T Y I C N V N H K P S N T  
 ^end of heavy chain, start of leucine zipper

2001 AAGGGTGCACA AGAAAAGTGA GCCCAAATCT TGTGACAAA CTCACGGCCG CATGAACAG CTAGAGGACA AGGTGAAAGA GCTACTCTCC AGAAACTAC  
 TTCCAGCTGT TCTTTCAACT CGGGTTAGA ACACTGTTT GAGTGGCCGGC GTACTTGTGTC GATCTCCGTG TCCAGCTCT CGATGAGAGG TTCTGTGATGG  
 213 K V D K K V E P K S C D K T H G R M K Q L E D K V E E L L S K N Y H  
 ^end of heavy chain, start of leucine zipper

2101 ACCTAGAGAA TGAAGTGGCA AGACTCAAA AACTGTCTGG GAGGCCGG AAGCTTAGTGT GCGGTTGGCTC TGGTTCCGGT GATTGATT ATGAAAAGAT  
 TGGATCTCTT ACTTCACCGT TTGACAGCTT TCTGAGTTT CGTGAACAGCC CTCGGGCC CCTGAATCAC CGCCACCCGAG ACCAAGGGCA CTAAAGCTAA TACTTTCTA  
 247 L E N E V A R L K K L V G E R G K L S G G S G D F D Y E K M  
 end of leucine zipper, start of gene III coat protein (267-end)

2201 GGCAAAACGCT AATAAGGGGG CTATGCCGA AAATGCCGAT GAAAACGGC TACAGTCTGA CGCTAAAGGG AACACTTGATT CTGTCGCTAC TGATTACGGT  
 CCGTTTTCGCA TTATTCCCCC GATACTGGCT TTTACCGCTA CTTTTCGCGG ATGTCAGACT GGCAATTTCGG TTGTAACCAA GACAGCGATG ACTAATGCCA  
 280 A N A N K G A M T E N A D E N A L Q S D A K G K L D S V A T D Y G

2301 GCTGCTATCG ATGGTTTCAT TGGTGAACGTT TCCGGCCTTG CTAATGGTAA TGCTGCTACT GGTCGATTTCG CTGGCTCTAA TTCCCAAATG GCTCAAGTCG  
 CGACGATAGC TACCAAAGTA ACCACTGCCA AGGGCGAAC  
 313 A A I D G F I G D V S G L A N G N G A T G D F A G S N S Q M A Q V G

2401 GTGACGGTGA TAATTCACT TTAAATGAAATA ATTCCGTCA ATATTCACT TCCCTCCCTC AATTCGGTTGA ATGTCGGCCCT TTGTCCTTA GCGCTGGTAA  
 CACTGCCACT ATTAAGTGGAA ATTAACTTAAAGGCAGT TAAAGGCAGT  
 347 D G D N S P L M N F R Q Y L P S L P Q S V E C R P F V F S A G K

2501 ACCATATGAA TTTCTATG ATTGTGACAA AATAAACTTA TTCCGGGGT TCTTTCGGTT TCTTTCGGTT ATTTCTACG ATTATCTACG  
 TGGTATACCT AAAAGATAAC TAACACTGTT TTATTTGAAT AACCTACCTT AACAGGGGAA AGAAAATAAA AATACATACA TAAAGATGC  
 380 P Y E F S I D C D K I N L F R G V F A F L L Y V A T F M Y V F S T

2601 TTTGGCTAACAA TACTGGCTAA TAAGGAGTCT TAATCATGCC AGTTCTTIG GCTAGGGCCG CCCTATACCT TGTCTGCCCT CCCGGTGTGC GTGGGGTGC  
 AACAGATGTT ATGACGCATT ATTCCCTAGA ATTAGTAGG  
 413 F A N I L R N K E S O

2701 ATGGAGCCGG GCCACCTCGA CCTGAATGGA AGCCGGGG ACCTGCTAA CGGATTCACC ACTCCAAGAA TTGGAGCCAA TCAATTCTTG CGGAGAACCTG  
 TACCTCGGCC CGGTGGAGCT GGACTTACCT TCGGCCGCC TGAGGGATT GCCTTAAGTGG TGGAGGGTT AACCTGGTT AGTAAAGAAC GCCTCTTGAC

2801 TGAATGGCA ACCAACCCCT TGGCAGAACAA TATCCATCGC GTCCGGCATC TCCAGCAGCC GCAACGGGG CATCTGGGG AGCGTTGGGT CCTGGCCACG  
 ACTTTACGGGT TTGGTTGGGA ACCGTTCTGT ATAGGTAGCG CAGGGGTAG AGGTGCTCGG CGTGGGCCCG GTAGAGCCCC TCGAACACCA GGACGGGTGC

2901 GGTGGCGATG ATCGTGTCTC TGTGTTGAG GACCGGGCTA GGCTGGGG GTGTCGCTTAC TGTTAGCAG AATGAATCAC CGATACCGCA GCGAACGTGA  
 CCACGGGTAC TAGCACGAGG ACAGCAACTC CTGGCCGAT CGACCCGCC CAACGGATG ACCATATCGTC TTACTTAGTG GCTATGCGCT CGCTTGCACT

3001 AGCGGACTGCT GCTGCAAAAC GTCTGGCACC TGAGCAACAA CATGAATGTT CTTGGTTTC CGTGGTTCTC AAAGTCTGGA AACGGGAAAG TCAGGGCCT  
 TCGTGTGACGA CGACGTTTIG CAGACGCTGG ACTCGTTGT GTACTTACCA GAAGCCAAAG GCACAAAGCA TTTCAAGACCT TTGCGCCCTC AGTCGGGGA

3101 GCACCAATT GTCCGGATC TGCATCGAG GATGCTGCTG CCTAACCTGT GGAACACCTA CATCTGTATT AACGAAGGCC TGGCATTGAC CCTGAGTGAT  
 CGTGGTAATA CAAGGCCTAG ACGTAGGTC CTACGAC CGATGGAC CCGTGTGGAT GTAGACATAA TTGCTTCGGC ACCGTAACTG GGACTCACTA  
  
 3201 TTTTCTCTGG TCCCAGCGCA TCCATACCGC CAGTGTTTA CCCTCACAAAC GTTCCAGTAA CCGGGCATGT TCATCATCG TAACCCGTAT CGTGAGCATC  
 AAAAGAGACC AGGGGGCGT AGGTATGGC GTCAACAAT GGGAGTGTG CAAAGGTATT GCCCCGTACA AGTAGTAGTC ATTGGCATA GCACCTCGTAG  
  
 3301 CTCTCTCGTT TCATCGGTAT CATTACCCC ATGAAACAGAA ATTCCCGCTT ACACGGGCC ATCAAGTGAC CAAACAGGAA AAAACCGCCC TAAACATGGC  
 GAGGAGCAA AGTAGCCATA GTAATGGGG TACTGTCTT TAAGGGGAA TGTGCTCCG TAGTTCACTG GTTGTCTT TTTGGGGG ATTGTACCG  
  
 3401 CCGCTTTATC AGAACCCAGA CTTAACGCAA TCTGGAGAAC CTCACGGGC TGGACAGGGCA TGAACAGGGCA GACATCTGT AATCGCTCA CGACCAACCGCT  
 GGCAGAAATAG TCTCGGTCT GTAAATTGCGA AGACCTCTT GAGTGTCTCG ACCTGGCCCT ACCTGTCCGT CTGTAGACAC TTAGGAAAGT GCTGGTGGGA  
  
 3501 GATGAGCTTT ACGCAGGAT CGGGAAATTG TAAACGTTAA TATTGTGTTA AAATTGGGT TAAATTGGT TAAATATCAGC TCATTTTTA ACCAATAGGC  
 CTACTCGAAA TGGCGTCTA GGCCTTAAC ATTGCAATT ATAAACAT TTAAAGGCCA ATTAAAAAC AATTAGTCG AGTAAAAAT TGGTTATCCG  
  
 3601 CGAAATCGGC AAAATCCCTT ATAATCAA AGAATAGACC GAGATAGGGT TGAGTGTGTT TCACTGTGG AACAAGAGTC CACTATTTAA GAACGTGGAC  
 GCTT TAGCCG TTTAGGAA TATTAGTT TCTTATCTGG CTCTATCCA ACTCACAAAC AGTCAACAAAC TTGTTCTCAG GTGATAATT CTGACACTTG  
  
 3701 TCCAACGTCA AAGGGCGAA AACCGCTAT CAGGGCTATG GCCCACTACG TGAACCATCA CCCTAACTAA GTTTTTGGG GTCCAGGGTC CCTAAAGGCAC  
 AGGTGCACT TCCCAGCTT TTGGAGATA GTCCGATAAC CGGGTGTATGC ACTTGGTAGT GGGATTAGT CAAAAACCC CAGCTCCACG GCATTTCGTRG  
  
 3801 TAAATCGGA CCTAAAGGG AGCCCCGAT TTAGAGCTTG ACGGGAAAG CGGGCGAACG TGGCGAGAAA GGAAGGGAG AAAGGAAAG GAGCGGGCGC  
 ATTATGCCCTT GGATTTCCC TCGGGGCTA AATCTCGAAC TGGCCCTTTC GGCCGCTTC ACCTGCTCTT CTTCCCTTC TTGCTTTT CTCGCCGGG  
  
 3901 TAGGGGCTG GCAAGTGTAG CGGTCAAGCT GCGGTAAACC ACCACACCCG CCGGCCCTAA TGCGCCGCTA CAGGGCGGT CGGATCTG CTCGCCGGCT  
 ATCCCGCGAC CGTCACATC GCGAGTGCAG CGCCGCAATT ACGGGGCGAT GTCCCGCCCA GGCCTAGGAC CGACGGCGCA  
  
 4001 TTGGGTGATG ACGGTGAATAA CCTCTGACAC ATGGAGCTCC CGGAGACGGT CACAGCTGT CTGTAAGGGG ATGCCGGGG CAGACAAGCC CGTCAGGGCG  
 AAGCCACTAC TGCCACTTT GGAGACTGT TACGTGAGG GCCTCTGCA GTGTGAAACA GACATTGCC TACGGCCCTC GTCTGGTGG GCAAGTCCCG  
  
 4101 CGTCAGCGGG TTGTTGGGG TGTCGGGG CAGCCATGAC CCAGTCACGT AGCGATAGGG GAGTGTATAAC TGGCTTAAC ATGGCCATC AGAGCAGATT  
 GCAGTCGCC ACAAACGCC ACAGCCCCG GTCCGGTACTG GTTCGATCGC CTCACATATG ACCGAATGTA TACGGCGTAG TCTCGTCTAA

4201 GTACTGAGAG TGCACCATAT GCGGTGTGAA ATACCGCACA GATGCGTAAG GAGAAAATA CGCATCGGC GCTCTTCGGC TTCCCTCGTC ACTGACTCGC  
CATGACTCTC ACCTGGTATA CGCCACACTT TATGGCGTGT CTACGGATTCT CTCTTTATG GCGTAGTCG CGAGAAGGGCG AAGGGGGAG TGACTGAGCG

4301 TGGGCTGGT CGTTCGGCTG CGGGGAGGG TATCAGCTCA CTCAAAGGG GTAATACGGT TATCCACAGA ATCAGGGAT AACGGAGAA AGAACATGTG  
ACGGAGCCA GCAAGGCCA GCGCTCGCC ATAGTCGAGT GAGTTTCCGC CATTATCCA ATAGGTCT TAGTCCCTA TTGCTCCCT TAGTGTACAC

4401 AGCAAAGGC CACCAAAGG CCAGGAACCG TAAAAAGGCC CGGTGTGCTGG CGTTTTCCA TAGGCTCCGC CCCCCTGACG ACCATCACAA AAATCGACGC  
TGTTTCCG GTCTGGTTCC GGTCCTGGC ATTTCGGG CGAACGAC GCAAAAGGT ATCGAGGGC GGGGACTGTC TCGTAATGTT TTAGCTGCG

4501 TCAAGTCAGA GGTTGGCAA CCCGACAGGA CTATAAAGAT ACCAGGGGT TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA  
AGTTCACTC CCACCGCTTT GGCGTGTCTT GATATTCTA TGGTCCGCAA AGGGGACCT TGAGGGAGC ACGGAGAGG ACAAGGCTGG GACGGCGAAT

4601 CGGGATACCT GTCCGGCTTT CTCCCTCGG GAAGGGTGGC GCTTCTCAT AGCTCAAGCT GTAGGTATCT CAGTTGGT TAGGTCTG TAGGTCTG  
GGCCTATGGA CAGGGAAA GAGGGAAACCTT CTCGGACCG CGAAAGAGTA TCGAGTGGCA CATCCATAGA GTCAAGGCCAC ATCCAGGAAG CGAGGTTCGA

4701 GGGCTCTGTG CACCGACCCC CGGTTCAAGG CGACCGCTGC GCCTTATCG GAACTATCG TCTTGAGTCC AACCCGGTAA GACACGACTT ATGCCACTG  
CCCGACACAC GTGCTTGGGG GGCAAGTGG CGTGGCGACG CGGAATAGGC CATTGATAGC AGAACTCAGG TTGGCCATT CTGTTGAA TAGGGTGA

4801 GCAGCAGCCA CTGCTAACAG GATTAAGAGA GCGGAGGTATG TAGGGGGTGC TACAGAGTTG TTGAAGTGGT GGCCCTAACTA CGGGTACACT AGAAGGAG  
CGTCGCTGGT GACCAATTGTC CTAATCGCT CGCTCCATAC ATCCGCCAG ATGCTCAAG AACTCACCA CGGATTGAT GCCGATGTGA TCTTCCTGTC

4901 TATTCTCAT CTGCGCTCTG CTGAAGGCAG TTACCTTCGG AAAAGAGT GTAGCTCTT GATCCGGCAA ACAAAACCAC GCTGGTAGCC GTGGTTTTT  
ATAAACATA GACGGGAGAC GACTTCGGTC AATGGAAGCC TTTTCTCAA CCATGAGAA CTAGGCCGT TGTTGGTGG CGACCATCGC CACCAAAAAA

5001 TGTTGCAAG CAGGAGATA CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGG TCTGACGGTC AGTGGAACGA AAACTCACGT  
ACAAACGTTIC GTCTCTAAT CGGGCTCTTT TTTTCTAGA GAACTAGAA AAGATGCCCG AGACTGGCAG TCACCTTGCT TTGAGTGCA

5101 TAAGGGATT TGCTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCTT TTTAAATTAA AAATGAAGTT TAAATCAAT CTAAGTATA TATGAGTAAA  
ATCCCTAA ACCAGTACTC TAATAGTTT TCCCTAGAT GGAATCTAGGA AAATTAAATT TTACTTCAA AATTTAGTT GATTTCATAT ATACTCATTT

5201 CTGGGTCTGA CAGTACCAA TGCTTAATCA GTGAGGCACC TATCTCAGGC ATCTGTCTAT TTGTTCTAC CATACTGCC TGACTCCCC TGTTGTAGAT  
GAACCAAGACT GTCAATGGT ACGAATTAGT CACTCCGTGG ATAGAGTCGC TAGACAGATA AAGCAAGTAG GTATCACGG ACTGAGGGC AGCACATCTA

5301 AACTACGATA CGGGAGGGCT TACCATCTGG CCCCACTGGT GCAATGATA CGCGGAGACCC ACGGCTCACCG GCTCCAGATT TATCAGCAAT AAACCAGCCA  
 TTGATGCTAT GCCTCCCGA ATGGTAGACC GGGGTCACGA CGTTACTATG GCGCTCTGGG TGGGAGTGGC CGAGGTCTAA ATAGTCGTTA TTGCGTCCGGT  
  
 5401 GCCGGAAAGGG CGGAGCGAG AAGTGGCTCT GCAAACCTTAT CCGGCCTCCAT CCAGTCCTATT AATTGTTGCC GGGAAAGCTAG AGTAAGTACT TCGCCAGTGA  
 CGGCCCTTCCC GGCTCGCGTC TTACCCAGGA CGTTCAGATA GGGGAGGTTA GGTCAAGATAA TTAAACAACGG CCCTTCGATC TCATTCATCA AGGGTCAAT  
  
 5501 ATAGTTTGCG CAACGTTGTT GCCATTGCTG CAGGCCATCGT GGTGTCACGC TCGTCGTTG GTATGGCTTC ATTCAAGCTCC GGTTCCAAC GATCAAGGGC  
 TATCAAACGC GTTGCACCAA CGGTAACGAC GTCCGTAGCA CCACAGTGGC AGCAGAAAC CATAACCGAAG TAAGTCGAGG CCAAGGGTTG CTAGTCCGGC  
  
 5601 AGTTACATGA TCCCCCATGT TGTGCAAAA AGCGGTTAGC ICCTTICGGTC CTCCGATCGT TGTCAGAAAGT AAGTGGCCG CAGTGTATTC ACTCATGTT  
 TCAATGTAATGACT AGGGGGTACA ACACGTTTT TCGCCAATCG AGGGTAGCA AGGAAGCCAG AACAGTCCTCA TTCAACCGGC GTCAACAATAG TGAGTACCAA  
  
 5701 ATGGCAGGCAC TGCCATAATTCTCTTACTGTC ATGGCATATCCG TAAGATGCTT TTCTGTTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC  
 TACCGTCGTG AGCTTAAAG AGAATGACAG TACGGTAGGC ATTCTACGAA AAGACACTGA CCACTCATGA GTGGTTCA GTAAGACTCTT ATCACATAGC  
  
 5801 GGCGACCGAG TTGCTCTTGC CGGGGTCAA CACGGGATAA TACCGGCCA CATAGCAGAA CTTAAAGT GCTCATCATT GGAAAACGTT CTTCGGGGCG  
 CCGCTGGCTC AACGAGAACG GGCGCAAGT GTGCCCTATT ATGGCGGGT GTATGCTCTT GAAATTTCAGA CGAGTAGTAA CCTTTGCAA GAAGCCCCGC  
  
 5901 AAAACTCTCA AGAGATCTTAC CGCTGTTGAG ATCCAGTTCG ATGTAACCCA CTCTGGCACC CAACTGATCT TCAGCCTCTT TTACTTTCAC CAGCGTTTCT  
 TTTGAGAGT TCCTAGAAAGC TAGGTCAAGC TACATTGGGT GAGCAGTGG GTGTGACTAGA AGTCGTGAA AATGAAAGTG GTCGCAAAAGA  
  
 6001 GGGTGAGCAA AACAGGAAG GCAAATGCC GCAAAGGG GAAATAAGGG GACACGGAA TGTTGAATAAC TCATACTCTT CCTTTTCAA TATTATTTGAA  
 CCCACTCGTT TTGTCCTTC CGTTTACGG CGTTTTTCC CGTATCCG CTTATTCCCG CTGTCCTT ACAACTTATG AGTATGAGAA GGAAAAGTT ATAATAACTT  
  
 6101 GCATTATCA GGTTATGT CTCATGGCG GATACATATT TGAATGTTT TAGAAAAATA AACAAATAGG GTTCCGGC ACATTCCCC GAAAAGTGCC  
 CGTAAATAGT CCAATAACA GAGTACTGC CTATGATAA ACTYACATAA ATCTTTTAT TTGTTTATCC CCAAGGGCG TGTAAGGGG CTITTCACGG  
  
 6201 ACCTGACGTC TAAGAAACCA TTATTACAT GACATTAACC TATAAAATA GGCGTATCAC GAGGCCCTT CGCTTCAAT ACAGTAGAC CTTTCGTAGA  
 TGGACTGCAG ATTCTTTGGT AATAATGTA CTGTAATTGG ATATTTTAT CCGCATAGTG CTCCGGAAA GCAGAAGTTA TGTCATCTG GAAAGGCATCT  
  
 6301 GATGTACAGT GAAATCCCG AAATTATACA CATGACTGAA GGAAGGGAGC TCGTCATTCC CTGCGGGTT ACGTCACCTA ACATCACTGT TACTTTAAA  
 CTACATGTCA CTTAGGGGC TTAAATATGT GTACTGACTT CCTTCCCTCG AGCAGTAAGG GACGGCCCAA TGCAGTGGAT TGTAGTGCATA ATGAAATT

6401 AAGTTTCCAC TTGACACTT GATCCCCTGAT GGAAAACGCA TAATCTGGGA CAGTAGAAG GGCCTCATCA TATCAAATGC AACGTACAAA GAATAGGGC  
 TTCAAGGTG AACTGTGAA CTAGGGACTA CCTTTGCGT ATTAGACCT GTCATCTTC CGGAAGTGT ATAGTTACG TTGATGTT CTTATCCCG

6501 TTCTGACCTG TGAAGCAACA GTCAATGGGC ATTGTATAA GACAAACTAT CTCACACATC GACAAACCA TACAATACAG GTAGACCTT CGTAGAGATG  
 AAGACTGGAC ACTTCGTGT CAGTTACCG TAAACATATT CTGTTGATA GAGTGTAG CTGTTGGTT ATGTTATGTC CATCTGGAA GCATCTCAC

6601 TACAGTGAAA TCCCCGAAT TATACACATG ACTGAAGGAA GGGAGCTCGT CATTCCCTGC CGGTTACGT CACCTAACAT CACTGTACT TTAAAAAAGT  
 ATGTCACCTT AGGGGCTTA ATATGTGTAC TGACTTCCTT CCCTCGAGCA GTAAAGGAGC GCCAATGCA GTGACAAATGA AATTTTTTCA

6701 TTCCACTTGA CACTTGTAC CCTGATGAA AACGCCATAAT CTGGGACAGT AGAAAGGCT TCATCATATC AAATGCAAGC TACAAAGAAA TAGGGCTTCT  
 AAGGTGAATG GTGAAACTAG GGACTACCTT TTGGGTATTA GACCCCTGTCA TCTTTCCGA AGTACTATAG TTGAGTGTGC ATGTTTCCTT ATCCCCGAAAGA

6801 GACCTGTGAA GCAACAGTCA ATGGGCATT GTATAAGACA AACTATCTCA CACATGACA AACAAATACA ATCTACAGT AGACCTTCG TAGAGATGTA  
 CTGGACACTT CGTGTCACT GTGTTAGACTT TACCCGTAA CATATTCTGT TTGATAGAGT GTGTTAGCTGT TTGTTATGT TAGATGTCCA TCTGAAAGC ATCTCTACAT

6901 CAGTGAATC CCCGAAATT TACACATGAC TGAAAGGAGG GAGCTCGTCA TTCCCTGCCG GTTACGTCA CCTAACATCA CTGTTACTTT AAAAAGTT  
 GTCACTTAG GGGTTTAAT ATGTCATG ACTTCCTCC CTCGAGCAGT AAGGGAGGC CCAATGCACT GGATTGTAGT GACAATGAAA TTTTTCAA

7001 CCACTTGACA CTTTGACATCCC TGATGGAAA CGCATAATCT GGGACAGTAG AAAGGGCTC ATCATATCAA ATGCAACGTA CAAAGAAATA GGGCTTCTGA  
 GGTGAACCTGT GAAACTAGGG ACTACCTTT GCGTATTAGA CCCTGTCACT TTCCCGAAG TAGTATAGT TACGTTGCAT GTTTCTTAT CCCGAAGACT

7101 CCTGTGAAGC AACAGTCAT GGGCATTTGT ATAAGACAAA CTATCTCACCA CATCGACAAA CCAATACAAT C  
 GGACACTTCG TTGTCAGTTA CCCGTAACAA TATTCTGTGTT GATAGAGTGT GTAGCTGTT GGTATGTTA G

1 ATGAAAAGA ATATCGCAT TCTTCTTGCA TCTATGTTCG TTTTTCTAT TGCTACAAT GCCTATGGAG ATATCCAGAT GACCCAGTCC CCGAGCTCC  
 TACTTCTCT TATAAGGTAA AGAAAGACGT AGATACAAGC AAAAAGATA ACCGATTTA CGGATACGTC TATAAGGTCTA CTGGGTCTAGG GGCTCGAGG  
 1 M K N I A F L L A S M F V F S I A T N A Y A D I Q M T Q S P S S L  
 ^met  
 ^start of signal sequence

^start of still signal sequence

101 TGTCGCCCTC TGTCGGCAT AGGGTCACCA TCACCTGCC TGCCAGTOAG GATGTCAG CTGCTGTCCA CTGGTATCAA CAGAAACAG GAAAAGCTCC  
 ACAGGGAG ACACCCGGCTA TCCCAGGGT AGTGGACGGC ACGGTCAGTC CTACACAGGT GACCATAGT GACCATAGT GTCTTGGTC CTTTCGAGG  
 35 S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P  
 ^CDR-L1

^CDR-L1

201 GAAGGTTCTG ATTAACTCGG CATCCTCTCCT CTACTCTGGA GTCCCTCTC GCTTCTCTGG TAGCCGGATT TCACTCTGAC CATCAGCAGT  
CTTCGAGAC TAAATGGCC GTAGGAAGGA GATGAGACCT CAGGGAAAGAG CGAAGAGACC ATGCCAAGG CCTGCTCAA AGTGGAGACTG GTAGTCGTC  
 68 K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S S  
 ^CDR-L2

^CDR-L2

301 CTGCAGCCGG AAGACTTCGC AACTTATTAC TGTCAAGCAAC ATTAACTAC TCCTCCACG TTCCGACAGG GTACCAAGGT GGAGATCAA CGAACTGTGG  
 GACGTCGGCC TTCTGAAGGG TTGAATAATG ACAGTCGTTG TAATATGATG AGGGGGTGC AAGGACAC CCTCTAGTT GCTTGACACC  
 101 L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T V  
 135 A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A  
 ^CDR-L3

^CDR-L3

401 CTGCACCATC TGTCTTCATC TTCCGCCAT CTGATGAGCA GTTGAATCT GGAACCTGCCT CTTGCTGTAAT AACCTCTATC CCAGAGAGC  
 GACGTGGTAG ACAGAAGTAG AAGGGGGTA GACTACTGT CAACTTTAGA CCTTGACGGA GACAACACAC GGAGGACTTA TGTAAAGATAG GGTCCTCTCG  
 135 A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A  
 168 K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S

501 CAAAGTACAG TGGAAAGGTGG ATAACGCCCT CCAATGGGT AACTCCAGG AGAGTGTCACTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC  
 GTTTCATGTC ACCCTCCACC TATTGCGGG A GTTAGGCCA TGAGGGTCC TCTCACAGTG TCTCGTCCCTG TGTTTCCCTGT CGTGGATGTC GGAGTCGTCG  
 168 K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCG CGAAGTCACC CATCAGGGCC TGAGGCTGCC CGTCACAAAG AGCTTCACACA  
 TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTGTTGTTTC AGATGGCAC GCTTCAGTGG GTAGTCAGTCG ACTCGAGCGG GCAGTGTTC TCGAAGTGT  
 201 T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R

**FIG.\_27A**

701 GGGGAGAGTG TGGTGCAGC TCCGGTATGG CTGATCGAA CCGTTCCGC GGTAAGGACC TGGCATTAACG CGAGGTGAT CCTCTACGCC GGACGCATCG  
CCCCCTCTCAC ACCACGGTCG AGGCCATAC GACTAGGCTT GCAAAGGC CCATTCCTGG ACCGTATTGA GCTCCGACTA GGAGATGGG CCTGGTAGC  
235 G E C G A S S G M A D P N R F R G K D L A O

^end of light chain, start of gd tag

801 TGGCCCTAGT ACCGAAAGT ACCTAAAG GGTAACTAGA GGTGAGGTG ATTATATGAA AMAGAATATC GCATTTCTTC TTGCACTAT GTTGTGTTTT  
ACCGGGATCA TGCGTTCAAG TGCAATTTC CCAACTCCAC TAAAATACTT TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA  
-23 M K K N I A F L L A S M F V F

^start of stII

901 TCTATTGCTA CAAACGGTA CGCTGAGGT CAGCTGGTGG AGTCTGGGG TGGCCTGGTG CAGCAGGGG GCTCACTCCG TTTGTCTGT GCAGCTCTG  
AGATAAACGAT GTTGGCAT GCGACTCCA GTCGACACC TCAGACCCAC ACCGGACAC GTCGGTCCCC CGAGTGGCC AAACAGGACA CGTGAAGAC  
-8 S I A T N A Y A E V Q L V S G G G L V Q P G G S L R L S C A A S G ^CDR-H1

^start of heavy chain

1001 GCTTCACCAT TAGTGGTCTP TGGTACACTT GGGTGGTCA GGCCCCGGT AAGGGCTGG ATGGGTIGC TGGATTTGCT CCTTATAGG GCGCTACTGA  
CGAAGGGTA ATCCAAGA ACCTATGTGA CCCACGGACT CGGCCCCCA TICCGGGACC TTACCCAAAG AJACCTAACGA GGAATATCGC CGCGATGACT  
27 F T I S G S W I H W V R Q A P G K G L E W V A W I A P Y S G A T D ^CDR-H2

^CDR-H3

1101 CTATGCCGAT AGCGTCAAGG GCCGTTTCAC TATAAGGCA GACACATCCA AAAACACAGC CTACCTACAA ATGAAACAGCT TAAGAGCTGA GGACACTGCC  
GATAACGGCTA TCGCAGTCC CGGCAAGTG ATATTGCGT CTGTGTAGGT TTTGTCTCG GATGGATGTT TACTGTGACT ATTCTGACT CCTGTGACGG  
60 Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T A

1201 GTCTTATT GTGCAAGAGA GGGGGCTTG TACTGGGTGT TCGACTACTG GGGTCAAGGA ACACTAGTCA CGCTCTCCTC GGCTCTCACC AAGGGCCAT  
CAGATAATAA CACGGTCTCT CCCCCCGAAC ATGACCCACA AGCTGATGAC CGCAGTCTCT TGTGATCAGT GGCAGAGGG CGGGAGGTGG TTCGGGGTA  
93 V Y Y C A R E G G L Y W V F D Y W G Q G T L V T V S S A S T K G P S ^CDR-H3

1301 CGGTCTTCCC CCTGGCACCC TCCCTCCAAGA GCACCTCTGG GGGCACAGGG GCCCTGGGT GCCTGGTCAA GAAGTACTTC CCCGAACCGG TGACGGTGTG  
GCCAGAAGGG GGACCGTGGG AGGAGGTCT CGTGGAGACC CCCGTGTCGC CGGGACCCGA CGGACCAAGT CCTGATGAAG GGGCTGGCC ACTGCCACAG  
127 V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V S

**FIG.-27B**

1401 GTGGAACCTCA GGGGCCCTGA CCAGGGGGGT GCACACCTTC CCGGCTGTC TACAGTCTC AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCTCTC  
 CACCTTGACT CCCGGGACT CGTGGCCCA CGTGGAAAG GGCGACAGG ATGTCAGGAG TCCTGAGATG AGGGAGTCTG CGCACCACTG GCACGGAGG  
 160 W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S

1501 AGCAGCTTGG CGACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG GTGACAAGA AAGTTGAGCC CAAATCTGT GACAAAAACTC  
 TCGTGAAACC CGTGGCTCTG GATGTAGACG TTGCACTTAG TGTTGGTTC CACGTGTTCT CTTAGAACAA CGTGTGAG  
 193 S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H

1601 ACCTCGTGG CGGTGGCTCT GGTTCGGTG ATTTGATTA TGAAAAGATG GAAACGCTA ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGCCGT  
TGGACTACC GCCACCGAGA CCAAGGCCAC TAAAACTAAT ACTTTTCTAC CGTTGGAT TATTCCCCCG ATACTGGCTAC TTACGGCTAC TTTTGGCGGA  
 227 L S G G S G S G D F D Y E K M A N A N K G A M T E N A D E N A L

^end of heavy chain

^start of gene III coat protein (267-end)

1701 ACAGTGTAC GCTAAAGGCA AACTGTACT GATTACGGT CTGCTATCGA TGGTTCTATT GGTCACGTTT CCGGCCCTGC TAATGGTAAT  
 TGTCAGACTG CGATTCCGT TTGAACTAAG ACAGGGATGA CTAATGCCAC GACGATAGCT ACCAAAGTAA CCACGCACTA TTAAAGTGGAA ATTACCATTA  
 260 Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L A N G N

1801 GGTGCTACTG GTGATTTCGC TGGCTCTAAT TCCCAAATGG CTCAGTCTGG TGACGGGTAT ATTICACCTT TAATGAATAA TTTCCGTCAA TATTTACCT  
 CCACGATGAC CACTAAACG ACCGAGATTA AGGGTTTACCGT GAGGTTCAACG ACTGCGCACTA TTAAAGTGGAA ATTACTTAAAGGCAGTT ATAAATGGAA  
 293 G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S

1901 CCCTCCCTCA ATCGGGTGAA TGTGCCCTT TTGTCTTAG CGCTGGTAA CCATATGAAT TTCTATTGA TTGTGACAA ATAAACTTAT TCCGGGGTGT  
 GGGAGGGAGT TAGCCAACCT ACAGGGGAA AACAGAAATC GGCACCAATT GGATACTTA AAGATAACT AACACTGTT TATTGAATA AGGCACCA  
 327 L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N L F R G V

2001 CTTTGGTTT CTTTTATATG TTGCCACCTT TATGTATGTA TTTCTACAT ACTGGCTAAAT AAGGGAGTCTT AA  
 GAAACGAA GAAATATAC AACGGTGAA ATACATACAT AAAGATGCA AACGATGTA TGACGGCATTA TCCCTCAGAA TT  
 360 F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

1 ATGAAAAGA ATATGCCATT TCTTCTTGCA TCTATGTTCG TTTTTTCATAT TGCTACAAAT GCCATGCAG ATATCCAGAT GACCAGTC CCGAGCTCCC  
 TACTTTCT TATAGGTAA AGAAGAACGT AGATACAAGC AAAAGATA ACAGATTTA CGGATACGTC TATAGGTCTA CTGGTCAGG GGCTCGAGGG  
 1 M K K N I A F L L A S M F V F S I A T N A Y A D I Q M T Q S P S S L  
 ^met  
 ^start of stII signal sequence

101 TGTCGGCCTC TGTTGGCGAT AGGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTGTCAG CTGGCTGTAGC CTGGTATCAA CAGAACAG GAAAAGCTCC  
 ACAGGGGGAG ACACCCGCTA TCCCAAGGGT AGTGGACGGC ACGGTCAAGTC CTACACAGGT GACGACATCG GACCATAGT GTCTCTGGTC CTTTCGAGG  
 35 S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P  
 ^CDR-L1

201 GAAGCTCTCTG ATTACTCGG CATCCTTCCT CTACTCTGGA GTCCCTTCCTC GCTTCTCTGG TAGCGGATT TCACCTGTAC CATCAGCAGT  
 CTTCGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAAG CGAACAGAAC ATGCCAAGG CCTTGCCAAAGG AGTGAGACTG GTAGTCGTC  
 68 K L L I Y S A S F L Y S G V P S R F S G S G T D F T L T I S S  
 ^CDR-L2

301 CTGCAGCCGG AAGACTTCGC AACTTATAC TGTCAGCAAC ATTATACTAC TCCCTCCACG TTGGACAGG GTACCAAGG GGAGATCAA CAACTCTATC  
 GACGTTGGCC TTCTGAAGGG TTGAATATAG ACAGTCGTTG TAATATGATG AGGGGGTAG CCTTGACGG AAGGGGTGC AAGCCTGTCC CATGGTCCA CCTCTAGTTT GCTTGACACC  
 101 L Q P E D F A T Y Y C Q H Y T T P P T F G Q G T K V E I K R T V A  
 ^CDR-L3

401 CTGCACCATC TGTCCTTCATC TTCCCGCCAT CTGATGAGCA GTGAAATCT GGAACCTGCCT CTGGCTGTGTG CCTGCTGAAT AACTCTATC CCAGAGGGC  
 GACGTTGGTAG ACAGAAAGTAG AAGGGGGTA GACTACTGTT CAACTTAA CCTTGACGG GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG  
 135 A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A

501 CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT ACTCCAGG AGACTGTCAC AGGAGGGAC AGCAAGGACA GCACCTACAG OCTCAGCAGC  
 GTTTCATGTC ACCITCCACC TATTGGGGA GTTAGGCCA TCTCACAGTG TCTGTCCTG CGTGGATGTC GGAGTCGTC  
 168 K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAG TCTACGCCCT CGAAGTCACC CATCAGGGCC TGAGCTGCC CGTCACAAAG AGCTTCAACA  
 TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTTTC AGATGGGAC CCTTCAGTGG GTAGTCCCTG GCAGTGGGG ACTCGAGGG GCAGTGGTTC TCGAAGTTGT  
 201 T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R

**FIG.-28A**

701 GGGGAGAGTG TGGGCCAGC TCCGGTATGG CTGATCGAA CGGTTTCGGC GGTAAAGGACC TGGCATTAACT CGAGGCTGAT CCTCTACGCC GGACGCATCG  
 235    G   E   C   G   A   S   S   G   M   A   D   P   N   R   F   R   G   K   D   L   A   O  
             ^end of light chain, start of gd tag

801 TGGCCCTAGT ACGGAAGTTC ACGTAAAAAG GGTAACTAGA GGTGAGGGTG ATTTATGAA AAAGAAATTC GCATTCTTC TTGCATCTAT GTTCGTTTTT  
 ACCGGGATCA TGCGTTCAAG TGCATTTC CCAACTCCAC TAATACTTCTT TAGT CGTCTTATAG AACGTAGATA CAAGCAAAA  
 -23  
             M   K   K   N   I   A   F   L   L   A   S   M   F   V   F  
             ^start of stII

901 TCTATTGCTA CAAACGGTA CGCTGAGGT CAGCTGGTGG AGCTCTGGGG TGGCTGGTG CAGCCAGGGG GCTCACTCCG TTTGTCTGTC GCAGCTTCTCG  
 AGATAACGAT GTTGGCAT GCGACTCCAA GTCACTCCAA TCAGACCCAC ACCGGACCC ACGCCGGCC CGAGTGGCC AAACAGACA CGTGAAAGAC  
 -8   S   I   A   T   N   A   Y   A   E   V   Q   L   V   S   G   G   L   V   Q   P   G   G   S   L   R   L   S   C   A   A   S   G  
             ^start of heavy chain

1001 GCTTCACCAT TAGTAATTAT GGGATAACACT GGGTGGTCA GGGCCGGGT AAGGGCTGG AATGGGTGG TAGGATTTCT CCTCTAAACG GCTCTACTTA  
 CGAACGGTA ATCATTAATA CCCCTATGTGA CCCACGCAGT CCGGGCCCA TTCCGGACC TTACCCAACC ATCCTAAAGA GGAAGATTGC CGAGATGAAT  
 27   F   T   I   S   N   Y   G   I   H   W   V   R   Q   A   P   G   K   G   L   E   W   V   G   R   I   S   P   S   N   G   S   T   Y  
             ^start of CDR-H2

1101 CTATGCCGAT AGCGTCAGG GCCGGTTCAC TATAAGGCA GACACATCCA AAAACACAGC CTACCTACAA ATGAAACAGCT TAAGAGCTGA GGACACTGCC  
 GATACGGGCTA TCGCAGTTC CGGCAAAGT ATATTCGGT CTGTGTAGT TTTGTGTCGA ATTCTGTGACT CCTGTGACGG  
 60   Y   A   D   S   V   K   G   R   F   T   I   S   A   D   T   S   K   N   T   A   Y   L   Q   M   N   S   L   R   A   E   D   T   A  
             ^CDR-H3

1201 GTCTTATTGT GTGCAAAAATG CTCGGTCAGG TTCGCTTACT GGGGTCAAGG AACACTAGTC ACCGGTCTCC CGGGCTCCAC CAAGGGCCA TCGGTCTCC  
 CAGATAATA CACGGTTAC GAGCCAGTCC AAGCGATGA CCCCAGTTCC TTGTGATCAG TGGCAGAGGA GCCGGAGGT GTTCCGGGT AGCCAGAAGG  
 93   V   Y   C   A   K   C   S   V   R   F   A   Y   W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S   V   F   P  
             ^CDR-H3

**FIG.\_28B**

1301 CCTTGGCACC CTCTCCAAG AGCACCTCTG GGGCACAGC GCCCCTGGGC TGCCTGGTCA AGGACTACTT CCCGAACCG GTGACGGTGT CGTGGAACTC  
 GGGACCGTGG GACGACCTTC TCCTGGAGAC CCCGGTGTGCG CCGGACCCG ACCGACCTT TCCATGATGAA GGGCTGGC CACTGCCACA GCACCTTGAG  
 127 L A P S S K S T S G T A A L G C L V K D Y F P E P V T V S W N S

1401 AGGGGCCCTG ACCAGCCCCG TGACACCTT CCCGGCTGTC CTACAGTCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CGGTGCCCTC CAGCAGCTTG  
 TCCGGGGAC TGCTGGCG ACGTGGAA GGGCGACAG GATGTCAGGA GTCTGAGAT GAGGGAGTC TCGCACCACT GGCAACGGG GTCGTGAAC  
 160 G A L T S G V H T F P A V L Q S S G L Y S L S V V T V P S S S L

1501 GGCACCCAGA CCTACATCTG CAACGTGAAT ACAAGCCCCA GCAACACCAA GGTGACAAAG AAAGTTGAGC CCAAATCTG TGACAAAAT CACCTICAGTG  
 CGCTGGCTGCTG GGTGACTA GTGTTGGGT CGTGTGGTC TTGCAACTCG GGTTAGAAC ACTGTTGAG ACTGTTGAG GTGGAGTCAC  
 193 G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H L S G ^end of heavy chain

start of gene III coat protein (267-end) ^

1601 GCGGTGGCTC TGGTTCGGT GATTGATT ATGAAAAGAT GGCACACCGT AAATAAGGGG CTATGACCGA AAATGCCAT GAAAACGGC TAGACTCTG  
 CGCCACCGAG ACCAAGGCCA CTAAACTAA TACTTTCTA CCGTTGGCA TTATCCCCC GATACTGGCT TTTACGGCTA CTTTGCGCG ATGTCAGACT  
 227 G G S G S G D F D Y E K M A N A N K G A M T E N A D E N A L Q S D

1701 CGCTAAAGGC AACTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG ATGGTTCTAT TGGTGCACGT TCCGGCTTG CTAATGGTAA TGGTGCCTACT  
 CGGATTCCG TTGAAACTAA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAGTA ACCACTGCCA AGGCCGGAAC GATTACCAT ACCACCATG  
 260 A K G K L D S V A T D Y G A A I D G F I G D V S G L A N G N G A T

1801 GGTGATTGCTGGCTCTAA TTCCCAATG GCTCAAGTGTG TAATTCACT TTAATGAAATA ATTTCGCTCA ATATTACCT TCCCTCCCTC  
 CCACTAAAC GACCGAGATT AAGGGTTTAC CGAGTCAGC CACTGCCTACT ATTAAAGTGGAA ATTACTTAAAGGAGT TATAAATGGA AGGGAGGGAG  
 293 G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S L P Q

1901 ATCGGTGTA ATGTCGCCCT TTTCCTTAA ACCATGAA TTTCATG ATTGTGACAA AATAAACTTA TTCCTGGTGT TCTTTCGCTT  
 TTAGCCAACCT TACAGGGGA AAACAGAAAT CGGCACCAT TGGTAACTT AAAAGATAC TAACACTGT TTATTTGAAT AAGGACCCAC AGAAACGCAA  
 327 S V E C R P F V F S A G K P Y E F S I D C D K I N L F R G V F A F

2001 TCTTTTATAT GTTGGCACCT TTATGTATGT ATTTCCTACG TTGCTAACAA TACTGGTAA TAAGGAGTCT TAA  
 AGAAAATATA CAACGGTGGAA AACACATACA TAAAGATGC AAACGATTGT ATGACGCAATT TCCCTCAGA ATT

360 L L Y V A T F M Y V F S T F A N I L R N K E S O

**FIG.-28C**

1 ATGAAAAGA ATATCGCAATT TCCTCTTGCA TCTATGTTCG TTTTTCTAT TGCTACAAAT GCCTATGCCAT CCGATATCCA GATGACCCAG TCCCCGAGCT  
 TACTTTTCT TATAGCGTAA AGAAGAACGT AGATAAACGC AAAAGATA ACGATGTTTA CGGATACGTA GGCTATAGGT CTACTGGTC AGGGGCTCGA  
 1 M K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S  
 ^met  
 ^start of stII signal sequence  
 ^light chain start

101 CCCTGTCGC CGCTGTGGC GATAGGGTCA CCATCACCTG CGGTGCCAGT CAGGATGTT CCACTGCTGT AGCCCTGGT CAACAGAAC CAGGAAAGC  
 GGGACAGGGC GAGACACCCG CTATCCCAGT GGTAGTGGAC GGCACGGTC GTCCTACACA GGTGACGACA TCGGACCATCA GTTGCTCTTG GTCCTTTTCG  
 35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A  
 ^CDR-L1

201 TCCGAAGCTT CTGATTTACT CGGCATCCTT CCTCTACTCT GGAGTCCTT CTGCTCTCTC TGGTAGCGGT TCCGGACGG ATTCACTCT GACCATCAGC  
 AGGCTTCGAA GACTAAATGAA GCCGTAGGAA GGAGATGAGA CTCAGGGAA GAGCGAAGAG ACCATGCCA AGGGCCCTGCC TAAAGTGAGA CTGGTAGTCG  
 68 P K L L I Y S A S F L Y S G V P S R F S G S G T D F T L T I S  
 ^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAA<sup>CTT</sup>TAC TACTGTCAGC ATCTTATAC TACTCTCCC AGCTTCCGAC AGGGTACCAA GGTGGAGATC AAACGAAC TG  
 TCAGACGTG GCCTCTGAA GCGTGTAAATAATAG ATGAGGAGGG TGAAGGCTG TCCCATGGTT CCACCTCTAG TTGCTCTGAC  
 101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V  
 ^CDR-L3

401 TGGCTGCACC ATCTGTCCTC ATCTTCCCGC CATCTGATGA CGAGTTGAAA TCTGGAACCTG CCTCTGTGT GTGCCCTGCTG AATAACTCT ATCCAGAGA  
 ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTT AGACCTGAC GGAGACAACA CACGGACGAC TTATGAAAGA TAGGGTCTCT  
 135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E  
 ^CDR-L3

501 GGCCAAAGTA CAGTGGAAAG TGATAAACGC CCTCCAATCG GTAACTCCC AGGAGAGTGT CACAGGGAG ACAGGACCTA CAGCCTCAGC  
 CCGGTTTCAT GTCACCTCC ACCTATTGG GGAGGTTAGC CATTTGGG TCCCTCTCACA GTGTCGTGTC CTGTCGTGGAT GTCGGAGTCG  
 168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S  
 ^CDR-L3

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACAA AAGTCTACGCC AGGAGACTAC ACCCATCAGG GCCTGAGCTC GCCCTCACA AAGAGCTTC  
 TCGTGGGACT GCGACTCGTT TCGTCTGTGT CTCTTGTGT TTCAGATGCC GACGCTCAG TGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT  
 201 S T L T L S K A D Y E K H V Y A C E V T H Q G L S S P V T K S F N

**FIG.\_29A**

701 ACAGGGAGA GTGTGGTGC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CGCGGTAAGG ACCTGGATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA  
 235    R    G    E    C    G    A    S    S    G    M    A    D    P    N    R    F    R    G    K    D    L    A    O  
     ^end of light chain, start of gd tag

801 TCGTGGCCCT AGTACCGAAG TTACCGTAAA AAGGGTAACT AGAGGGTAG GTGATTTTAT GAAAAGAAT ATGCCATTIC TTCTTGATC TATGTTGTT  
 AGCACCGGA TCATGGTTC AAGTGGATT TTCCCCATGA TCTCCAATC CACTAAATA CTTCCTTA TAGCGTAAAG AAGAACGTAG ATACAAAGCAA  
 -23

                        ^ start of stII

901 TTTCTATTG CTACAAACGC GTMACGCTGAG GTTCAGCTGG TGGAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGCTCACT CCGTTTGTCC TGTGAGCTE  
 AAAAGATAAC GATGTTGCG CATGGCACTC CAAGTCGACC ACCTAGAACCC GGCACCCGAC CACGTGGTC CCCGAGTGA GGAAACAGG ACACGTGAA  
 -9    F    S    I    A    T    N    A    Y    A    E    V    Q    L    V    E    S    G    G    G    L    V    Q    P    G    G    S    L    R    L    S    C    A    A    S  
     ^CDR-H1  
     ^start of heavy chain

1001 CTGGCTTAC CATTAGTGGT CTGTATATAC ACTGGGTCG TGAGGGCC TGAAATGGGT TGGTGGATT TCTCTTATG GCGGGAAATC  
 GACCGAAGTG GAAATACCA AGACTATATG TGACCCACGC AGTCGGGGC CAATTCCGG ACCTAACCA ACCATCTAA AGAGGAATAC CGCCGTTATG  
 26    G    F    T    I    S    G    S    D    I    H    W    V    R    Q    A    P    G    K    G    L    E    W    V    G    R    I    S    P    Y    G    N    T  
     ^CDR-H2

1101 TAATATGCC GATAGGGTCA AGGGCCGTT CACTATAAGC GCAGACACAT CAAAAAACAC AGCTTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT  
 ATTGATAAGG CTATGGCACT TCCGGAAA GTGATATTCG CGTCTGTGA GTTTTGTG TGGAATGGAT GTTACTTGT CGAATTCTCG ACTCTGTGA  
 59    N    Y    A    D    S    V    K    G    R    F    T    I    S    A    D    T    S    K    N    T    A    Y    L    Q    M    N    S    L    R    A    E    D    T

1201 GCGGTCTATT ATTGTGCAAG AGTCGGGGC CTCAAGTGC TGTTGACTA CTGGGTCAA GGAACTAG TCACCGTCTC CTGGGCTCC ACCAAGGGCC  
 CGGCAGATAA TAACACGGTC TCAGCCGGCG GAGTTCAACG ACAAGCTGAT GACCCAGT CCTTGIGATC AGTGGAGAG GAGGCCGAGG TGGTICCCGG  
 92    A    V    Y    C    A    R    V    G    G    L    K    L    F    D    Y    W    G    Q    G    T    L    V    T    S    S    A    S    T    K    G    P  
     ^CDR-H3

1301 CATCGGTCTT CCCCTGGCA CCCTCTTCCA AGAGCACCTC TGGGGCACA GGGCCCTGG GCTGCCCTGG CAAGGACTAC TTCCCCGAAC CGGTGACGGT  
 GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGACCG CGACGGACCA GTTCTGTATG AAGGGGTTG GCCACTGCCA  
 126    S    V    F    P    L    A    P    S    S    K    S    T    S    G    G    T    A    A    L    G    C    L    V    K    D    Y    F    P    V    T    V

1401 GTCGTGGAAC TCAGGGCCC TGACCAGGG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGGGTGGT GACCGTGCC  
 CAGCACCTTG AGTCCGGGG ACTGGTCCGCC GCACGTGGG AAGGGCCGAG AGGATGTCAG GAGTCCTGAG ATGAGGGAGT CGTCGCACCA CTGGCACGG  
 159 S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P

1501 TCCAGGAGCT TGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGGC CAGCAACACC AAGGTCGACA AGAAAGTGA GCCCAAATCT TGTGACAAAA  
 AGGTGGCGA ACCCGTGGGT CTGGATGTAG ACGTGCACT TAGITGCACT GTGTTGCGG TTCAGCTGT TCTTCGACT CGGGTTAGA ACACGTGTT  
 192 S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T

1601 CTACAGCCG CATGAAACAG CTAGAGGACA AGGTGAAAGA GCTACTCTCA AAGAACCTACC ACCTAGAGAA TGAAGTGGCA AGACTCAAAA AACATGTCGG  
 GAGTGGGGC GTAGTTGTC GATCTCCGTG TCCAGCTTCT CGATGAGAGG TTCTTGATGG TGGATCTCT ACTTCACCGT TCTGAGTTT TTGAAACAGCC  
 226 H G R M K Q L E D K V E E L L S K N Y H L E N E V A R L K K L V G  
 ^ end of heavy chain, start of leucine zipper

1701 GGAGCGGGA AACCTTAGTG GCGGTGGCTC TGTTTGGGT GATTGGTATG ATGAAAGAT GGCAAACGGT AATAACGGG CTATGACCGA AAATGCCGAT  
 CCTCGGGCCT TTGGAATCAC CGCCACGGAG ACCAAGGCCA CTAAGCTAA TACTTTCTA CGGTTGGCA TTATCCCCC GATACTGGCT TTTACGGCTA  
 259 E R G K L S G G S G D F D Y E K M A N K G A M T E N A D  
 ^ end of leucine zipper, gene III coat protein (267-end)

1801 GAAACCGCG TACAGTCTGA CGCTAAAGGC AAAACTTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG ATGTTTCAT TGGTACGTT TCCGGCCTTG  
 CTTTGGCG ATGTCGAGCT GCGATTCCG TTGAACTAA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAGTA ACCACTGCAA AGGCCGAAAC  
 292 E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L A

1901 CTAATGGTAA TGGTGGCTACT GGTGATTTG CTGGCTCTAA TTCCCAAATG GCTCAAGTCTCG GTGACCGGTGA TAATTCACT TTAAATGAATA ATTTCGGCA  
 GATTACATT ACCACGATGA CCACTAAAC GACGGAGATT AGGGTTTAC CGAGTTCAGC CACTGCCACT ATTAAGTGGAA ATTAACTTAT TAAAGGCAGT  
 326 N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N F R Q

2001 ATATTACCT TCCCCCTC AATCGGTGA ATGTCGCTCTA GCGCTGGTA ACCATATGAA TTTTCATFTG ATTGTGACAA ATAAGACTTA  
 TATAATGGAA AGGGAGGGAG TTAGCCAACT TACAGGGGA AAACAGAAAT CGCGACATT TGGTATACTT AAACACTGTT TTATTGAAAT

359 Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N L

2101 TTCCGTGGTG TCTTGTGGTT TCTTTATAT GTTGGCCACCT TTATGTATGT ATTTCCTACG TTGCTAACAA TACTGGTAA TAAGGGAGTCT TAA  
 AAGGCACCAAGAAAATATA CAACGGTGGAA ATACATACA TAAAGATGC AAACGATGT ATTCTCTCAGA ATT

392 F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

**FIG.-29C**

1 ATGAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTCTAT TGCTTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCCGAGCT  
 TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAACATA ACGATGTTA CGGATACGTA GGCTATAGGT CTACTGGTC AGGGCTCGA  
 1 M K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S  
 ^start of stII signal sequence  
 ^met

101 CCCTGTCCGC CTCTGTGGC GATAGGGTCA CCATCACCTG CCGTGCAGT CAGGATGTGT CCACGTGTGT AGCCGTGGT CAACAGAAC CAGGAAAC CAGGAAAGC  
 GGGACAGGGCG GAGACACCCG CTATCCCAGT GGTAGTGGAC GGCACGGTCA GTCCCTACACA GGTGACGCCA TCGGACCATCA GTTGTCTTG GTCCTTTTCG  
 35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A  
 ^CDR-L1

201 TCCGAAGCTT CTGATTACT CGGCATCCTT CCTCTACTCT GGACTCCCTT CTCGCCTCTC TGCTAGGGT TCCGGACGG ATTCACTCT GACCATCAGC  
 AGGCTTCGAA GACTAAATGA GCGTAGGAA GGAGATGAGA CCTCAGGGAA GAGGGAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG  
 68 P K L L I Y S A S F L Y S G V P S R F S G S G T D F T L T I S  
 ^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTT TACTGTCAAC TACTCTCCG AATCTTATAC TACTCTCCG ACGTTGGAC AGGGTACAA GGTGAGATC AAACGAAC TG  
 TCAGACGTG GCCTTCTGAA GCGTTGAATA ATGACAGTCG TTAGAATTATG ATGAGGAGGG TGCAGGCC TCCCATGGTT CCACCTCTAG TTTGCTTGAC  
 101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V  
 ^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAACCTG CCTCTGTGT GTGCCTGCTG AATAACTCT ATCCCAAGAGA  
 ACCGACCGTGG TAGACAGAAG TAGAAGGGC GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATGAAAGA TAGGGTCTCT  
 135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGGAAAG TGATAAACGC CCTCCAAATCG GGTAACACTCC AGGAGAGTGT CACAGAGGAG ACAGGAAAG ACAGCACCTA CAGGCCCTCAGC  
 CCGGTTCAT GTCACCTCC ACCTATGCG GGAGGTTAGC CCATTGAGGG TCCCTCTCACA GTGCTCGTC CTGTCGTCC TGTCGTGGAT GTCCGGAGTCG  
 168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGCTACCGC CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCGTACA AAGAGCTCA  
 TCGTGGGACT GCGACTCGTT TCCTCTGTGT CTGTCGTGTT CGACTGTCAG TGGTAGTGCCT CGGACTCGAG CGGGCAGTGT TTCTCGAAGT  
 201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

**FIG.\_30A**

701 ACAGGGAGA GTGTGGTGC CAGCTCCGGTA TGGCTGATTC GAACCGTTTC CGCGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCCTCTAC GCCGGACGCA  
 TGTCCTCTCACACACACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAAG GGGCCATTIC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CGGCCCTGCGT  
 235 R G E C G A S S M A D P N R F R G K D L A O  
 ^ end of light chain, start of gd tag

801 TCGTGGCCCT AGTACCGAAG TTACGTAAA AAGGGTAACT AGAGGGTAG GTGATTTT GAAAAGAAT ATCGGATTC TTCTTGATC TATGTTCGTT  
 ACCACGGGA TCATGGTTC AACGTGCATT TTCCCATGA TCTCCAATC CACTAAATA CTTTTCTTA TAGCGTAAG AAGAACGTAG ATACAAGCAA

-23

M K K N I A F L L A S M F V  
 ^ start of still  
 4 9 1 A T N A Y A E V Q L V E S G G G L V Q P G G S L R L S C A A S  
 ^ start of heavy chain  
 1001 CTGGCTTCACTTAACTTAC ACTGGGTGCG CACTATAAGC GCAGGACACAT CAACTACCA CAAATGAACA GCTTAAGGAGC TGAGGACACT  
 GACCGAAGTG GAAATGATTA AGGCTATATG TGACCCACGC AGTCGGGGC CATTCCGG ACCTTACCCA ACAGATGATAA ATAGGAATAC CGAATTCTCG ACTCTGTGA  
 26 G F T I T N S D I H W V R Q A P G K G L E W V A T I Y P Y G G Y T  
 ^ start of H1

1101 TTACTATGCC GATAAGGTCA AGGGCCGTTT CACTATAAGC GCAGGACACAT CAACTACCA CAAATGAACA GCTTAAGGAGC TGAGGACACT  
ATGATACGG CTATGCCAGT TCCGGCAA GTGATATTCG CGTCGTGTA GTTCTTGTG TCGGATGGAT GTTACTGT CGAATTCTCG ACTCTGTGA  
 59 Y Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T  
 ^ start of H2

1201 GCCGCTTATT ATTGTGCAAG AGGGGGGGG ATGGACGGCT ACGTATGGA CTACTGGGT CAAGGAACAC TAGTCACCGT CTCCCTCGGCC TCCACCAAGG  
 CGGAGATTA TAACACGTTC TCCCCGGCC TACCTGCGGA TGCAATACTT GATGACCCCA GTTCTTGTG ATCAAGTGGCA GAGGAGCCGG AGGTGGTCC  
 92 A V Y Y C A R G G M D G Y V M D Y W G Q G T L V T V S S A S T K G  
 ^ start of H3

1301 GCCCCTCGGT CTCCCCCTG GCACCCCTCCT CCAAGAGCAC CTCTGGGGC ACAGGGGGC TGGGCTGCCT GGTCAGGAC TACTTCCCCG AACCGGTGAC  
 CGGGTAGCCA GAAGGGGGAC CGGGGGAGGA GTTCTCGTG GAGACCCCG TGTGCGGGG ACCGACGGGA CCAGTTCCTG ATGAAGGGGG TTGGCCACTG  
 126 P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T

1401 GGTGCTGGG AACTCAGGG CGCTGACCA GGGCGTGCAC ACCTTCCGG CTGCTTACA GTCTCAGGA CTCTACTCCC TCAGGAGCG TGACCGTG  
 CCACAGCAC TTAGCTCCGC GGGACTGGTC GCCGCACGTG TGGAAAGGGC GACAGGATGT CAGGAGTCCT GAGATGAGGG AGTCGTCGCA CCACTGGCAC  
 159 V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V

1501 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACAA GCCAGCAAC ACCAAGGTCG ACAAGAAAGT TGAGCCCCAA TCTTGTGACA  
 GGGAGGTGGT CGAACCCCGT GGTCGAGT TAGACGTTGC ACTTAGTGTG CGGGTCTTGC TGGTCCAGC TGTTCTTCA ACTCGGGTT AGAACACTGT  
 192 P S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K

1601 AAACTCACGG CCCATGAAA CAGCTAGGG ACAAGGTGCA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAAGCTTGT  
 TTGAGTGCC GGCGTACTTT GTCGATCTCC TGTTCAGCT TCTCGATGAG AGGTTCTTGA TGGTGGATCT CCTACTTCAC CGTCTGAGT TTTTGAACA  
 226 T H G R M K Q L E D K V E L L S K N Y H L E N E V A R L K K L V

^end of heavy chain, start of leucine zipper

1701 CGGGAGGC GAAAGCTTA GTGGCGTGG CTCTGGTCC GGTGATTGG ATTATGAAA GATGCAAAC GCTAATAAGG GGGCTATGAC CGAAAATGCCC  
 GCCCCTCGCG CCTTCGAAT CACCGGCCACC GAGACCAAGG CCACTAAAC TAATACTTTT CTACCGTTTG CGATTATTCC CCCGATACTG GCTTTTACGG  
 259 G E R G K L S G G S G D F D Y E K M A N A N K G A M T E N A

^end of leucine zipper, start of gene III coat protein (267-end)

1801 GATGAAACG CGCTACAGTC TGACGCTAAA GGGAAACTTG ATTCTGTCGC TACTGATTAC GGTGCTGCTA TCGATGGTTT CATGGGTGAC GTTTCGGCC  
 CTACTTTCG GCGATGTCAG ACTGCGATT CCCTGGTGAAC TAAGACAGGC ATGACTAATG CCACGACGAT AGCTACCAA GTAACCACTG CAAGGGCCGG  
 292 D E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L

1901 TTGCTATGG TATGGTGT ACTGGTGT ATTACCAAG AACGACCGAG ATTAAGGGT TACCGAGTTC AGCACTGCG ACTATTAAGT GGAAATTACT TATTAAGGC  
 AACGATTAAC ATTACCAAGA TGACCAACTAA AACGACCGAG ATTAAGGGT TTGCTGGCTC TAATTCCCAA ATGGCTCAAG TGCTGACGG TGATAATTCA CCTTTAATGA ATAATTCCG  
 326 A N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R

2001 TCAATATTAA CCTCCCTCC CTCAAATGGGT TGAATGTCG CCTTTGGTCT TTAGGCGTGG TAAACCATAT GAATTTCATA TTGATGTTGA CAAAATAAAC  
 AGTTATAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGCG GGAAAACAGA AATCGGCACC ATTGGTATA CTAAAGAT AACTAACACT GTTTTATTIG  
 359 Q Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N

2101 TTATTCCGTG GTGCTTGC GTTTCTTTA TATGGTGCCTA CCTTTATGTA TGTATTCT ACGTTGGCTA ACATACTGCG TAATAAGGAG TCTTAA  
 AATAAGGCAC CACAGAACG CAAAGAAAT ATACAAACGGT GGAAAACAGA AATCAAAGAT ACATAAAAGA TGOAAACGT ATTATTCCTC AGAATT  
 392 L F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

1 ATGAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTGC TTTTCTAT TGCTACAAAT GCTATGCCAT CCGATATCCA GATGACCCAG TCCCCGAGCT  
 TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAGATA ACCGATGTTA CGGATACGTA GGCTATAGGT CTACTGGTC AGGGGCTCGA  
 1 M K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S  
 ^met ^light chain start

101 CCCGTCCGC CTCTGTGGC GATAGGTCA CCATCACCTG CGGTGCCAGT CAGGATGTT GTTCCACTGCTGT AGGCCTGGT CAACAGAAC CAGGAAAGC  
 GGGACAGGGC GAGACACCCG CTATCCAGT GGTAGTGGAC GGCACGGTC GTCCTACACA GTGGACGACA TCGGACCATA GTTGCTTGT GTCCTTTTCG  
 35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A  
 ^CDR-L1

201 TCCGAAGCTT CTGATTACT CGGCATCCTT CCTCTACTCT GGACTCCCTT CTCGCTTCTC TGGTAGGGT TCCGGACGG ATTACTCT GACCATCAGC  
 AGGCTTCGAA GACTAAATGA GCCGTAGGA GGAGATGAGA CTCAGGGAA GAGGGAAAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG  
 68 P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S  
 ^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTT TACTGTCAAGC ATCTTATAC TACTCTCCC ACGTTGGAC AGGGTACAA GGTGAGATC AACGAACTG  
 TCAGACGTCG GCCTCTGAA GCGTTGAATA ATGACAGTCG ITAGAAATATG ATGAGGAGGG TGGAAAGCCTG TCCCATGTT CCACCTCTAG TTGCTTGTGAC  
 101 S L Q P E D F A T Y C Q Q S Y T T P P T F G Q G T K V E I K R T V  
 ^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCGC CATCTGATGA GCAGTTGAA ACTGCTGCTG CCTCTGTGT GTGCCTGCTG AATAACTCT ATCCAGAGA  
 ACCGACGTGG TAGACAGAAG CCTCCTACTC AGACCTGTGAC GGAGACAAACA CACGGACAC TTATGAAAGA TAGGGTCTCT  
 135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGGAAAG TGGATAAGC CCTCCACTCC AGGAGACTGT CACAGAGGAG ACAGCACCTA CAGCCCTCAGC  
 CCGGTTTCAT GTCACCTTCC ACCTATTGGC GGAGGTAGC CCATTGAGGG TCCTCTCACA GTGTCCTGTC CTGTCGTCC TGTCGTGGAT GTCGGAGTTCG  
 168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGCT GCCGTACACA AGAGGCTCA  
 TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTGTGT TCGTGTGTT GACGCTTCAG TGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT  
 201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

**F/G.-31A**

701 ACAGGGAGA GTGTTGGGCC AGCTCCGGTA TGGCTGATCC GAACCGTTC CGGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCCTCAT GCCGGACGCA  
 TGTCCTCTCACACCACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAAG GCGCCATTCC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CGGCCTGCGT  
 235 R G E C G A S S G M A D P N R F R G K D L A O  
 ^ end of light chain, start of gd tag

801 TCGGGCCCT AGTACGCCAG TTACACGTAAA AAGGGTAACT AGAGGTGAG GTGATTTTAT GAAAAGAAT ATCGCATTC TCTCTGCATC TATGGTCGTT  
 ACCACGGGA TCATGGTTC AAGTGCATT TTCCCATGA TCTCAACT CACTAAATA CTTTTCTTA TAGCGTAAG AAAGAACGTAG ATACAAGCAA  
 -23 M K K N I A F L L A S M F V  
 ^ start of stII

901 TTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGGTGG TGGAGTCTGG CGTGGCCTG GTGCAGCCAG GGGGCTACT CGGTCTGTC TGTCAGCTC  
 AAAAGATAAC GATGTTGCG CATGCTGACTC CAAGTCGACC ACCTCAGACC GCCACGGAC CACGTGGTC CCCGAGTGA GGCAAAACAGG ACACGTCGAA  
 -9 F S I A T N A Y A E V Q L V E S G G C L V Q P G G S L R L S C A A S  
 ^ start of heavy chain

1001 CTGGCTCAC CATTAAATAAT TATGATAATAAC ACTGGTGGCG TCAGGCCCG GGTAAAGGGC TGGAAATGGGT TGGTTATATT TCTCCCTCCTA GCGGGCTAC  
1001 GACCGAAGTG GAAATTATAA ATACTATATG TGACCCACGC AGTCGGGGC CATTCCGG ACCTAACCA ACCAATATAA AGAGGAGAT CGCCGCCATG  
 26 G F T I N N Y D I H W V R Q A P G K G L E W V G Y I S P P S G A T  
 ^ start of heavy chain

1101 TTAATGCC GATAGCGCTCA AGGGCCGGTT CACTATAAGC GCAGACACAT CAAAAAACAC AGCCTAACCA CAAATGAACA GCTTAAGAGC TGAGGACACT  
 ATGATAACGG CTATGCCAGT TCCCGGCCAA GTGATATTCG CGTCTGTGA GTTGTGTA CGTTCTGTG ACCTCTGTG ACTCTGTGA  
 59 Y Y A D S V K G R F T I S A D T S R N T A Y L Q M N S L R A E D T

1201 GCCGCTATT ATTGTGCAAG AATGGTGGCG ATGGGGAGGG GGGTTATGGA CTACTGGGGT CAAGGAACAC TAGTCACCGT CTCCCTCGGC TCCACCAAGG  
 CGGCAGATMA TAACACGTTC TTACCAAGCCG TACGCCCTCCC CCCAATACCT GATGACCCCA GTTCCTGTG ATCACTGGCA GAGGAGCCGG AGGTGGTTCC  
 92 A V Y Y C A R M V G M R R G V M D Y W G Q G T L V T V S S A S T K G  
 ^ CDR-H3

1301 GCCCATCGGT CTTCCTCTG GCACCCCTCT CCAAGGAC CTCTGGGGC ACAGGGGGC TGGGCTGCT GGTCAAGGAC TACTTCCCCG AACGGGTGAC  
 CGGTAGCCA GAAGGGGGAC CGTGGGAGGA GTTCTCGTG GAGACCCCCG TGTGGCCGG ACCCGACGGA CCAGTCTCTG ATGAAGGGGC TTGGCCACTG  
 126 P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T

1401 GGTGTCGG AACTCAGGG CGCTGACAG CGGGTGCAC ACCTTCCGG CTGCTCTACA GTCTCAGGA CTCCTACTCCC TCAGGAGCGT GGTGACCGGT  
 CCACAGCAC TTAGTCCGC GGGACTGTC GCCGACCGTG TGGAAGGGCC GACAGGATGT CAGGAGTCT GAGATGAGGG AGTCGTCGCA CCACTGGCAC  
 159 V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V

1501 CCCTCOAGCA GCTTGGCAC CCAGACCTAC ATCTGCAACG TGAATCACAA GCCAGAAC ACCAAGGTCG ACAAGAAAGT TGAGCCCCAA TCTTGTGACA  
 GGGAGGTCT GTGAGCTGGATG TAGACGTTGC ACTTAGTGTG CCGGTCTGGT CAGGAGTCT GAGATGAGGG AGTCGTCGCA CCACTGGCAC  
 192 P S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K

1601 AAACTAACGG CGGCATGAAA CAGCTAGAGG ACAAGGTGCA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAACATTGT  
 TTGAGTGCC GGGTACTTT GTCGATCTCC TGTTCCAGCT TCTCGATGAG AGGTTCTAC CGTTCTGAGT TTTTTGAACA  
 226 T H G R M K Q L E D K V E E L L S K N Y H L E N E V A R L K K L V  
 ^end of heavy chain, start of leucine zipper

1701 CGGGAGGC GGAAGCTTA GTTGGGGTGG CTCGGTTCC GGTGATTGG ATTATGAAA GATGGCAAC GCTAAATAAGG GGGCTATGAC CGAAAATGCC  
 GCCCCTCGCG CCTTCTGAAT CACCGCCACC GAGACCAAGG CCACTAAAC TAATACTTT CTACCGTTTG CGATTATTC CCCGATACTG GCTTTACGG  
 259 G E R G K L S G G S G D F D Y E K M A N A N K G A M T E N A  
 ^end of leucine zipper

^gene III coat protein (267-end)

1801 GATGAAACG CGCTACAGTC TGACGCTAAA GGCAAACTTG ATTCTGTCGC TACTGATTAC GGTGCTGGCTA TCGATGGTTT CATGGTGCAC GTTTCGGCC  
 CTACTTTGCG GCATGTCAG ACTGCGATT CCGTTGAAC TAAGACAGG ATGACTATG CCACGACGAT AGCTACCAA GTAACCACTG CAAAGGCCGG  
 292 D E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L

1901 TTGGTATGG TAATGGTGT ACTGGTGT ATTACCAACG TGACCAAA AACGACCGAG ATTAAGGGT TACCGAGTTC AGCCACTGCC ACTTAAAGT GGAAATTACT TATTAAGGC  
 AACGATTAAC ATTACCAACG TGACCAAA AACGACCGAG ATTAAGGGT TACCGAGTTC AGCCACTGCC ACTTAAAGT GGAAATTACT TATTAAGGC  
 326 A N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R

2001 TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTCGC CCTTTGCTT TAACCATAT GAATTTCATA TTGATTTGTA CAAAATAAAC  
 AGTTATAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGCG GAAAACAGA ATTCGGCACC ATTIGGTATA CTAAAAGAT AACTAACACT GTTTTATTG  
 359 Q Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N

2101 TTATTCCGTG GTGTCCTTGC GTTGTCTTTA TATGGTGCCTA CCTTATGCA TGTATTCTCT ACCTACTGCG TAATAAGGAG TCTTAA  
 ATAAGGCAC CACAGAAAAG CAAAGAAAAT ATACAACGGT TGCAAAACGAT TGTATGACGC ATTATTCCCTC AGAATT  
 392 L F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

**FIG.-31C**

1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTATTTCAGG AAGCTTGGCC AAAAGAGAAGA AGAGTCGAAT  
 CTTAACCTTCA AGAGGTATGAA AACCTTCC TTATATGCTTG TACTTTTAG AGTAACGACT CAACAATAAA TTCAACGGG TTTTCTCTTCT TCTCAGCTTA  
  
 101 GAACTGTGT CGCAGGTAGA AGCTTGGAG ATTATCGTC CTGCAATGCT TCGCAATATG GCGCAAATG ACCAACAGCG GTTGTATTGAT CAGGTAGGG  
 CTTGACACAC GGTCCATCT TCAGAAACCTC TAATAGCACT GACGTAGCT AGCGTTACGA AGCGTATAC CGCGTTTAC TGGTGTGCC CAACTAACTA GTCCCATCTCC  
  
 201 GGGCGCTGTA CGAGGTAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GGATTAGCT AAAGAAAGTTA TTGAGGCATC CTCGTCAGTA  
 CCCGACAT GCTGCACTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTCTCTTAAT AACTTCGTA GAGCAGTCAT  
  
 301 AAAAGTTAAT CTTTCAACA GCTGTCAATAA AGTGTGTCAAG GCCGAGACTT ATAGTCGCTT TGTTTTATT TTAAATGTA TTGTAACTA GTACGCAAGT  
 TTTCAATTAA GAAAAGTTG CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCAGAA ACAAAAATAA AAATTCAT AACATTGAT CATGCGTTCA  
  
 401 TCACGTTAAA AGGGTATGTA GAGGTGAGG TGATTTATG AAAAGAAATA TCGCATTCTC ACTAAATAC TTTTCTTAT AGCGTAAAGA AGAACGTAGA TACAAGCAA AAAGATAACG ATGTTTACGG  
 ATGCACTTTCATCC ACTAAATAC TCCCAACTCC ACTAAATAC TTTTCTTAT AGCGTAAAGA AGAACGTAGA TACAAGCAA AAAGATAACG ATGTTTACGG  
 0 M K K N I A F L L A S M F V F S I A T N A  
 ^ start of stII signal sequence  
  
 501 TATGCAGATA TCCAGATGAC CCAGTCCCCG AGCTCCCTGT CGGCCTCTGT GGGCETAGG GTIACCATCA CCTGCCGTGC CAGTCAGGAT GTGTCACGT  
 ATACGTCTAT AGCTCTACTG GGTCTGGCTC TTGGTCTCTT TTGGCTCTT CGAAGACTAA ATGAGCGTA GGAGGGAGAT GAGACCTCAG GGAAGGCCA AGAGACCAC  
 21 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T A  
 ^ start of light chain  
 ^ EcorV  
  
 601 CTGTAGCCCTG GATCAACAG AAACCAAGAA AAGCTCCGAA GCTTCTGATT TACTGGCAT CCTTCCTCTA CTCTGGAGTC CCTCTCGCT TCTCTGGTAG  
 GACATGGAC CATAGTGTGTC TTGGTCTCTT TTGGCTCTT CGAAGACTAA ATGAGCGTA GGAGGGAGAT GAGACCTCAG GGAAGGCCA AGAGACCAC  
 55 V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S  
 ^ CDR-L2  
  
 701 CGGTCCGGG ACGGATTCA CTCTGACCAT CAGCAGTCTG CAGCCGGAA ACTTCGCAAC TTAACTACTGT CAGCAATCTT ATACTACTCC TCCCACGTC  
 GCCAAAGGCC TGGCTAAAGT GAGACTGGTA GTCGTCAGAC GTGGCCTTC TGAAGCGTTG ATTAATGACA GTCGTGTAGAA TATGATGAGG AGGGTGCAG  
 88 G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F  
 ^ CDR-L3

**FIG.\_ 32A**

801 CCAAGGGTA CCAAAACGA GATCAAACGA ACTGTGGCTG CACCATCTGT CTTCATCTTC CGGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCCTCTG  
 CCTGTCACCT CCTAGTTCACCT CTAGTTTGCT TGACACCGAC GTGGTAGACA GAAGTAGAAG GGCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGGAGAC  
 121 G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V  
 ^KpnI

901 TTGTTGCT GCTGAATAAC TTCTATCCA GAGAGGCCAA AGTACAGTGG AGGGTGGATA AGCCCTCCA ATCGGGTAAC TCCCGAGAGA GTGTCACAGA  
 AACACACCGA CGACTTATG AAAGATAGGGT CTCTCGTT TCATGTACC TTCCACCTAT TGCGGGAGGT TAGCCCCATG AGGGTCCCT AGAGTGTCT  
 155 V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E

1001 GCAGGACAGC AAGGACAGCA CCTACAGGCCT CAGCAGCAC CTGACGCTGA GCAAAGCAGA CTACGGAGAA CACAAAGTCT AGCCCTGGGA AGTCACCCAT  
 CGTCCTGTCG TTCCCTGTCGT GGATGTCGGA GTCGTCGTT GACTGCGACT CGTTTCGCTCT GATGCTCTTT GTGTTTCAGA TGCGGACGCT TCAGTGGTA  
 188 Q D S K D S T Y S L S S T L T L S K A D Y E R H K V Y A C E V T H  
 ^end of light chain, start of gd tag

1101 CAGGGCCCTGA GCTCGCCGT CACAAAGAGC TTCAACAGGG GAGAGTGG TGCCAGCTCC GGATATGGCTG ATCCGAACCG TTTCGGGGT AAGGACCTGG  
 CTTCCGGACT CGAGGGGGCA GTGTTTCCTCG AAGTTGTCCTCC CTCTCACACC AGCCTCGAGG CCATACCGAC TAGGGCTTGGC AAAGGGGCCA TTCCGGACC  
 188 Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L A  
 ^end of light chain, start of gd tag

1201 CATAACTCGA GGCTGATCCT CTACGCCGGA CGCATCGGG CCCTAGTACG CAAAGTCAAG TAAGAAGGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA  
 GTATTGAGCT CCGACTAGGA GATGCGGCCT GCGTAGCACC GGGATCATGC GTTCAAGTGC ATTTCCTCCA TTGATCTCCA ACTCCACTAA AATACTTTT  
 255 0  
 -23

M K K  
 ^start of stII  
 ~BsiWI

1301 GAATATCGCA TTTCCTCTTG CATCTATGTT CGTTTTTCT ATTGCTACAA AGCCGTACCC TGAGGTTCAG CTGGTGGAGT CTGGGGGGG CCTGGTGCAG  
 CTTATAGCGT AAAGAAGAAC GTAGATACAA GCAAAAAGA TAACGATGTT TGCGCATGGG ACTCCAAGTC GACCACCTCA GACCGCCACC GGACACGTC  
 -20 N I A F L L A S M F V F S I A T N A Y A E V L V E S G G G L V Q  
 ^start of heavy chain

**FIG.-32B**

1401 CCAGGGGGCT CACTCCGTTT GTCCCTGTGCA GCTTCTGGCT TCACCATTAG TGTTTCTTGG ATTACACTGGG TGCCTCAGGC CCCGGTAAG GGCCTGGAAAT  
 GGTCGGCGA GTGAGGGAAA CAGGACACGT CGAACGCCA AGTGGTAATC ACCAACACC TATGTGACCC ACGGAGTCGG GGGCCCATTC CGGACCTTA  
 14 P G S L R L S C A A S G F T I S G S W I H W V R Q A P G K G L E W  
 ^CDR-H1

1501 GGTTTGCTTG GATTGCTCCT TATAGGGGG CTACTGACTA TGGCGATAAC GTCAAGGGCC GTTTCACTAT AAGGGCAGAC ACATCCAAA ACACAGCCTA  
 CCCAACGAAC CTAACGAGGA ATATCGCGC GATGACTGAT AGGGCTATCG CAGTTCCGG CAAAGTGTATA TTTCGGCTCTG TGTAGGTTTT TGTGTCGGAT  
 48 V A W I A P Y S G A T D Y A D S V K G R F T I S A D T S K N T A Y  
 ^CDR-H2

1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATTATGG CAAGAGGGG GGGCTTGATGAC TGGGTGTCG ACTACTGGGG TCAAGGAACA  
 GGATGTTTAC TTGTCGAATT CTCGACTCCT GTGACGGCAG ATAATAAACAC GTTCTCTCCC CCCGAACATG ACCCCACAAGC TGATGACCCC AGTTCCTTGT  
 81 L Q M N S L R A E D T A V Y I C A R E G G L Y W V F D Y W G Q G T  
 ^CDR-H3

1701 CTAGTCACCG TCTCCCTGGC CTCCACCAAAG GGACCATCGG TCTTCCTCC GGACCCCTCC TCCAAGAGCA CCTCTGGGG CACAGCGGCC CTGGCTGCC  
 GATCAGTGGC AGAGGGCCG GAGGTGGTTCC CGGGTAGCC AGAACGGGCA CGCTGGAGG AGGTCTCTCGT GGAGACCCCC GTGTCGCCGG GACCCGACGG  
 114 L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C L  
 ^Apai

1801 TGGTCAAGGA CTACTTCCCC GAACGGGTGA CGGTGCGTG GAACTCAGGC GCCCTGACCA GGGCGTGCA CACCTTCCCG GCTGTCCTAC AGTCCTCAGG  
 ACCAGTTCTT GATGAAGGGG CTTGGCAACT GCCACAGCAC CTGAGTCCG CGGGACTCTGGT CGGGACTCAGT GTGGAAGGGC CGACAGGATG TCAGGAGTCC  
 148 V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G

1901 ACTCTACTCC CTAGCAGGGC TGGTGACCGT GCCCTCCAGC AGCTTGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCAGCAA CACCAAGGTC  
 TGAGATGAGG GAGTCGTGCG ACCACTGGCA CGGGAGGTGG TCGAACCCCGT GGTTCTGGAT GTAGACGTTG CACTTAGTGT TCGGTGCGTT GTGGTICAG  
 181 L Y S L S S V V T V P S S L G T Q T Y I C N V N H K P S N T K V

2001 GACAAGAAAG TTGAGCCCAA ATCTTGTGAC AAAACTCACC TCTAGAGTGG CGGTGGCTCT GGTTCCGGTG ATGCTGGTT GCCGGGGGC GTTTTTATG  
 CTGTTCTTTC AACTCGGGTT TAGAACACTG TTGAGTGG AGATCTCACC GCCACCGAGA CCAAGGCCAC TACGAGCAA CGGGCCCCG CAAAATAAC  
 214 D K V E P K S C D K T H L O

2101 CTAGGGCCGC CCTATACCTT GTCTGCCCTT CGCGTGCAC TCGAGGGGG CCACCTCGAC CTGAATGGAA GCCGGGGCA OCTCGCTAAC  
 GATCGGGGG GAGATATGGAA CAGACGGAGG GGCGAACAGC AGCGCCAGT ACCTGGCCCC GGTTGAGCTG GACTTACCTT CGGCGGCGT GAGGGCATTG

2201 GGATTCACCA CTCAGGAAAT TGGAGCCAAAT CAATTCTTGC GGAGAACTGT GAATGGCAA ACCAACCCCTT GGCAGAACAT ATCCCATCGG TCCGCCATCT CCTAAGTGGT GAGGTCTTTA ACCTCGGTAA GTAAAGAACG CCTCTTGACA CTTCAGCGTT TGGTGGAA CGCTCTTGTAA TAGGTAGCGC AGGGGTAGA

2301 CCAGCAGCCG CACGGGGCCG ATCTCGGGCA GCGTTGGGTC CTGGCCACGG GTGCCATGA TGCGTCCCT GTCGTGTAGG ACCCGGCTAG GCTGGGGGG GGTGTCGGC GTGGGCGGG TAGAGCCCGT CGCAACCCAG GACCGGGGCC CACGGTACT ACCGGTACT ACCGGAGGA CAGCCAGGA CAGCACCTCC TGCGCCGATC CGACCCGCC

2401 TTGCTTAATCT GCTTAGCAGA ATGAATCACC GATAACGGAG CGAACGTGAA CGCAGTGTG TGTGGCACCT TGCACAAAC ATGAATGGTC AACGGAATGA CCAATCGCTT TACCTAGTGG CTATGCGCTC GCTTGCACCT CGCTGACGAC GACGTTTGC AGACGTTGGA CTCGTTGTG TACTTACAG

2501 TTCGGTTTCC GTGTTTCTA AAGTCTGGAA ACGCGGAAGT CAGCGCCCTG CACCATATG TCCGGATCT GCATCGCAGG ATGCTGCTGG CTACCCCTG TG AAGCAGG CACAAAGG CACAAAGCAT TTCAAGACCTT TGCGCCTTCA GTCGGGGAC GTGGTAATAC AAGGCTTAA CGTAGCGTCC TAGGACGACC GATGGGACAC

2601 GAAACCTAC ATCTGTATA ACGAAGGGT GGCATTGACC CTGAGTGATT TTTCCTCTGGT CCCGCCGCAT CCATACCGCC AGTTGTTAC CCTCACAAACG CTTGTTGGATG TAGACATATT TGCTTGCAG CCGTAACCTGG GACTCAAA AAAGAGACCA GGGGGCGTA GGATGGGG TAGACAAATG GGAGTGTGCA

2701 TTCCAGTAAC CGGGCATGTT CATCATCAGT AACCCGTATC GTGAGCATCC TCTCTCGTT CATCGCTATIC ATTACCCCAGA TGAAACAGAAA TTCCCCCTTA AAGGTCAATTG GCCCGTAAAGA GTAGTGTCA TTGGGCATAG CACTCGTAGG AGAGGCAA GTAGCCATAG TAATGGGGGT ACTTGTCTT AAGGGGAAT

2801 CACGGGGCA TCAAGTGAAC AACAGGAAA AAACCGCCCT TAACATGCC CGCTTATCA GAAAGCCAGAC ATTAAACGCTT CTGGAGAAC TCAACGAGCT GTGCTCCGT AGTTCACTGG TTGTTCCCTT TTGGGGGA ATTGTACGG CGAAATAATGT CTTCGGCTCG TAATTGGGA GACCTCTTGT AGTTGCTCGA

2901 GGACGGGGAT GAAACAGGGAG ACATCTGTGA ATCGCTTCAC GACCACGTG ATGAGCTTCA CGCAGGATC CGGAATTGT AAACGTTAAT ATTTGTAA CCTGGCCCTA CTTCGCGTC TGTAGACACT TAGCGAAGTG CTGGTGGAC TACTGAAAT GGCCTCTAG GCCTTAACA TTGCAATT TAAACATT

3001 AATTCCGGTT AAATTCTGT TAAATCAGCT CATTCTTAA CCAATAGGCC AAATCCCTTA TAAATCAAAA GAATAGACCG AGATAGGGTT TTAAGGCAGA TTAAAAAAACA ATTAGTCGA GTAAAAAAATT GTTACGGAAAT ATTAGTTT CTATCTGGC TCTATCCAA

3101 GAGTGTGTG ACAAGAGTC ACATTTAAAG AACGTGGACT CCAACGTCAA AGGGGAAAC ACCGTCTATC AGGGCTATGG CCCACTACGT CTCACAAACAA GGTCAAACCT TTGTTCTCAGG TTGATAATTTC TTGCACCTGA GGTGCACTGC TTGGAGATAG TCCCAGTAAAC GGGTGTGCA

3201 GAACCATCAC CCTAATCAAG TTTTTGGG TCGAGGTGCC GTAAAGCCT AAATCGGAAC CCTAAAGGGA GCCCCCCGATT TAGAGCTTGA CGGGAAAGC  
CTTGGTAGTG GGATTAGTC AAAAACCCC AGCTCACGG CATTICGTGA TTAGGTCTTG GGATTTCCCT CGGGGGCTAA ATCTGAAC TCCCCTTTC  
3301 CGCGAACGT GGGGAAAG GAAGGAAAGA AAGGAAAGG AGGGGGCGCT AGGGGGCTGG CAAGTGTAGC GGTACGGCTG CGCGTAACCA CAACACCGGC  
GCCGCTTGC A CGCGCTTTC CTTCCCTCTT TCGCTTCC TCGCCCCCGA TCCCGCGACC GTTCACATCG CCAGTGCAC GCGCATTTGT GGTGTGGCG  
GCCGGAATTA CGCGGAGATG TCCCGCAG GCCTAGGACG GAGCGCGAA AGCCACTACT GCCACTTTTG GAGACTGTGT ACGTCGAGGG CCTCTGCCAG  
3401 CGCGCTTAAT GGGCGCTAC AGGGCGCTC CGGATCCTGC CTGGCGCTT TCGGGATGA CGGTAAAAC CTCTGACACA TGCAGGTCCC GGAGACGGT  
TGTGAAACAG ACATTGCGCT ACGGCCCTCG TCTGTCGGG CAGTCGGCG CAGTCGGCCA CAAACGCCA AGCCACTACT GCCACTTTTG GAGACTGTGT ACGTCGAGGG CCTCTGCCAG  
3501 ACAGCTTGTG TGTAAGGGA TGCCGGAGC AGAAAGCCC GTCAGGGCC GTCAGGGGGT GTAGGGGGT GTCCGGGGC AGCCATGACC CAGTCACGTA  
TGTGAAACAG ACATTGCGCT ACGGCCCTCG TCTGTCGGG CAGTCGGCG CAGTCGGCCA CAAACGCCA AGCCACTACT GCCACTTTTG GAGACTGTGT ACGTCGAGGG CCTCTGCCAG  
3601 CGGATAGGG AGGTATACT GGCTTAAC TA GAGCAGATG TACTGAGATG GCACCATATG CGGTGTGAAA TACCGCACAG ATGCGTAAGG  
CGCTATGCC TCACATATGA CGAATTGAT AGCGCTAGT CTCGCTAAC ATGACTCTCA CGTGGTATAC GCCACACTT ATGGGTGTC TAGCATTTC  
3701 AGAAAATACC GCATCAGGGC CTCTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGCT GTTCGGCTGC GGGGAGGGT ATCAGCTCAC TCAAAGGGGG  
TCTTTATGG CGTAGTCGGC GAGAGCGAGT GACTGAGCC CGCCAGCCAG CAAGGCCAGC CGGCTCGCCA TAGTCGAGTG AGTTTCGGCC  
3801 TAATACGGTT ATCCACAGAA TCAGGGATA ACAGATGTGA GAAACATGTGA GCAAAGGGCC ACCAAAAGGGC CAGGAACCGT AAAAAGGGCG CGTTGCTGGC  
ATTATGCCA TAGGTGTCTT AGTCCCTAT TGCTCCTT CTGTACACT CGTTTCCGG TCGTTTCCGG GTCTTGGCA TTTTCCGG CAAACGACCG  
3901 GTTTTCCAT AGGCTCCGCC CCCCTGACCA GCATCACAAA ATCGACCGT CAAGTCAGAG GTGGCGAAC CGCACAGGAC TATAAAGATA CAGGGCGTT  
AAAAAGGTA TCGAGGGGG GGGACTGCT CGTAGTGTGT TTAGCTGCGA GTTCAGTCTC CACCGCTTTTG GGCTGTCTG ATATTTCTAT GTCCGCAA  
4001 CCCCTGGAA GCTCCCTCCT GCGCTCTCGT CGGATACTAC CGGATACTCG TCCGCTTTTC TCCGCTCGGG AAGGCTGGC CTTTCTCAT  
GGGGACCTT CGAGGGAGCA CGCAGAGGA CAAGGAGGA CGCGAGGG ACCGGCAATG GCCTATGGAC AGGGGAAAGG AGGGAAAGCCC TTGCGACCGC GAAAGAGTAT  
4101 GCTCACGCTG TAGGTATCTC AGTCGGGT AGGTGGTG CTCACAGGTG GGTGTGTGC AGGAACCCC CGTTCAAGGGC GACGGCTGGC CCTTATCCGG  
CGAGTGCAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GACGTTCCAC CCGACACAGC TGCCTGGGG GCAAGTGGG CTGGCGACGC GAAATAGGCC  
4201 TAACTATCGT CTGAGTCCA ACCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGGCCAC TGCTAACAGG ATTAGGAG CGAGGTATGT AGGGGTGCT  
ATTGATAGCA GAACTCAGGT TGGCCATTG TGCTGAAT AGCGGTGACCG GTCTGCTGGTG ACCATGTCTC TAATCGTCTC GCTCCATACA TCGGCCACGA

4301 ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTAACACTA GAAGGACAGT ATTGGTATC TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTC  
TGTCCTAAGA ACTTCACCAC CGGATTGAT CCGATGTGAT CTTCCTGTCA TAAACCATAG ACGGAGACG ACTTCGGTCA ATGGAAGCCT TTTCTCAAC

4401 GTAGCTCTTG ATCCGGAAA CAAACCACCG CTGCTAGCCG TGGTTTTTT GTTGCAGAAC AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC  
CATCGAGAAC TAGGCCGTT GTTGGGGC GACCATCGCC ACCAAAAAA CAAACGTTCG TCGTCTAATG CGCGTCTTTT TTTCCTAGAG TTCTTCAGG

4501 TTTGATCTT TCTACGGGT CTGACGCTCA GTGCAACGAA AACTCACGGT AACTGCTT AAGGGATTG TTGTCATGAGA TTATCAAAA GGATCTTCAC CTAGATCCTT  
AAACTAGAAA AGATGCCCA GACTGGAGT CACTTGCTT TTGACTGCCA TTCCCCCTAAA CCAGTACTCT AATAGTTTTT CCTAGAAAGTG GATCTAGGAA

4601 TAAATTAAATATGAAGTT TAAAGTATAT ATGAGTAAC TTGGTCTGAC AGTTACCAAT GCTTAATTCAG TGAGGCACCT ATCTCAGCGA  
AATTAAATT TTACTTCAAA ATTAGTTAG ATTTCATAATA TACTCATTTG AACAGACTG TCAATGGTA CGAATTTAGTC ACTTCGGTGA TAGAGTCGCT

4701 TCTGTCATT TGTTCTTC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTTAGATAAC GGGAGGGCT ACCATCTGGC CCCAGTGCTG CAATGATACC  
AGACAGATAA AGCAAGTAGG TATCAACGGG CTGAGGGCA GCACATCTAT TGATGCTATG CCCTCCGAA TGTTAGACCG GGGTCACGAC GTTACTATGG

4801 GCGAGACCCA CGCTCACGG CTCCAGATT ATCAGCAATA ACCAGCCAG CGGGAAAGGGC CGAGGCAGA AGTGGTCTG CAACTTATC CGCTTCATC  
CGCTCTGGGT GCGAGTGGC GAGGTCAA TACTCGTTAT TTGGTGGTC GGCCTTCCCG GCTCGGTCT TCACCGGAC GTTGAATAG GGGAGGTAG

4901 CAGTCTATT ATTGTTGCCG GGAAGCTAGA GTAAAGTAGT CGCCAGTTAA TAGTTGGCG AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACCGCT  
GTCAGATAAT TAACAACGCC CCTTCGATCT CATTCATCAA GCGGTCAATT ATCAAACGCC TTGCAACAC GGTAACGACG TCCGTAGCAC CACAGTGCAG

5001 CGTCGTTGG TATGGCTCA TTCAAGCTCCG GTTCCCACCG ATCAAGGGCA GTTACATGAT CCCCATGTT GTGCAAAAAA GCGTTAGCT CCTCGGGTCC  
GCAGCAAACC ATACCGAAGT AAGTCGAGGC CAAGGGTTGC TAGTTCCGCT CAATGTACTA GGGGTACAA CACGTTTTT CGCCAATCGA GGAAGCCAGG

5101 TCCGATCGTT GTCAGAAGTA AGTGGCCGC AGTGTATCA CTCAATGGTTA TGGCAGGACT GCATAATTCT TTACTGCTCA TGCATCCGT AAGATGCTT  
AGGCTAGCAA CAGTCTTCAT TCAACGGCG TCACAAATAGT GAGTACCAAT ACCGTCTGA CGTATTAAGA GAATGACAGT ACGGTAGGA TTCTACGAA

5201 TCTGTTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAT AGTGTATGG GCGACCGAGT TGCTCTTGC CGCGGTCAAC ACGGATAAT ACCGGCGCAC  
AGACACTGAC CACTCATGAG TTGGTTCACT AAGACTCTTA TCACATACGC CGCTGGCTCA ACGAGAACGG GCCGAGTGG TGCCCTATT TGGCGGGTGA

5301 ATAGGAGAAC TTAAAAGTG CTCATCATG GAAACGTT TCGGGGGA AAACCTCAA GGATCTCAA CGTGTGAGA TCCAGTTCGA TGTAACCCAC  
 TATCGTCTG AATTTTCAC GAGTAGAAC CTTTGCAG AAGCCCCGCT TTGAGAGTT CCTAGAATGG CGACAACCT AGGTCAAGCT ACATTGGGTG  
 5401 TCGTGCACCC AACTGATCT CAGCATCTT TACCTTCACC AGCGTTCTG GGTGAGCAA ACAGGAAGG CAAGATGCCG CGACAACCT AGGTCAAGCT ACATTGGGTG  
 AGCACGTTGG TTGACTAGAA GTCGTAGAAA ATGAAAGTGG TCGCAAAGAC CCACTCGTT TGTCTTCGCT GTTTACGGC GTTTTCCC TTATTCGGC  
 5501 ACACGAAAT GTGAAATCT CATACTCTC CTTTCAAT ATTATGAG CATTATCAG GCCTATCAG GCTTATGTC TCAATGAGGG ATACATATT GAATGTTT  
 TGTGCCTTA CAACTTATGA GTATGAGAAG GAAAAGTAA TAATAACTC GAAATAGTC CCATAACAG AGTACTGCC TATGTATAA CTACATAAA  
 5601 AGAAAAATAA ACAAAATGGG GTTCCGGCA CATTCCCG AAAAGTGCAC CCTGACGCT AAGAAACCAT TATATCATG ACATTAACCT ATAAAAAATAG  
 TCTTTTATT TGTGTTATCCC CAAGGGCGGT GAAAGGGCC TTTTCACGGT GGACTGCCA TCTTGGTA ATAATAGTAC TGTAATGGG TATTTTATC  
 5701 GCGTATCAGC AGGCCCTTC GTCCTCAATA CAGGTAGACC TTGCTAGAG ATGTCAGTG AAATCCCGA AATTATCAC ATGACTGAAG GAAGGGAGCT  
 CGCATAGTGC TCCGGGAAAG CAGAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTCAC TTACGGGCT TTAATATGTG TACTGACTTC CTTCCCTCGA  
 5801 CGTCATTCCC TGCCGGTTA CGTCACCTAA CATCACTGTT ACTTTAAAAA AGTTCCACT TGACACTTTC ATCCCTGATG GAAAACGCAT AATCTGGGAC  
 GCACGAGGG AGGGCCCAAT GCAGTGATT GTAGTGACAA TGAATTTT TCAAGGTGA ACTGTCAAC TAGGGACTAC CTTTGGCTA TTAGACCTG  
 5901 AGTACAAAGG CCTTCATCAT ATCAAATGCA ACGTACAAG AAATAGGGCT TCTGACCTGT TGAACACTTG ATCCCTGATG GAAAACGCAT AATCTGGGAC  
 TCATCTTCC CGAAGTAGTA TAGTTACGT TGCTATGTTT  
 6001 TCACACATCG ACAAAACCAAT ACAATACAGG TAGACCTTC GTAGAGATGT ACAGTAAAT CCCGAAATT ATACACATGA CTGAAAGGAAG GGAGCTCGTC  
 AGTGTAGC TGTGGTTA TGTTATGTC ATCTGGAAAG CATCTCTACA TGTCACCTTA GAGCTGACA CTCGTTGTC AGTACCCGT AAACATATTC TGTGTGATAG  
 6101 ATTCCCTGCC GGGTACGTC ACCTAACATC ACTGTTACTT TAAAAAGTT TCCACTTGCAC ACTTTGATCC CTGATGGAAA ACGATAATC TGGGACAGTA  
 TABGGACGG CCCAATGAG TGGATGGTAG TGACAATGAA ATTTTTCAA AGGTGAACTG TGAAACTAGG GACTACCTT TGCGTATTAG ACCCTGTCAT  
 6201 GAAAGGGCTT CATCATATCA AATGCAACGT ACAAAAGAAT AGGGCTCTG ACCTGTGAAG CAAACGTCAA TGGGCAATTG TATAAGACAA ACTATCTAC  
 CTTCCCGAA GTAGTATAGT TTACGTGCA TGTTCTTTA TCCCGAAAGAC TGGACACTTC GTGTCAGTT ACCCGTAAAC ATATTCTGTT TGATAGAGTG  
 6301 ACATGACAA ACCAATACAA TCTACAGGT GACCTTCGT AGAGATGTC AGTGAATTC CGAAATTAT ACACATGACT GAAGGAAGGG AGCTCGTCAT  
 TGTAGCTGTT TGGTTATGTT AGATGTCCTAT CTGAAAGCA TCTCTCATG TCACCTTAGG GGCTTAAATA TGTGTACTGA CTTCTTCCC TCGAGCAGTA  
 6401 TCCCTGCCG GTTACGTCAC CTAACATCAC TGTACTTTA AAAAAGTTT CACTGACAC TTGATCCCT GATGGAAAAC GCATAATCTG GGACAGTGA  
 AGGCAGGGCC CAAATGCAAGTG GATTGTAAGT ACATGAAT TTTTCAAG GTGAACTGTT AACTAGGG CA TACCTTTG CGTATTAGAC CCTGTCACTT  
 6501 AAGGGCTTCA TCATATCAA TGCAACGTAC AAAGAAATAG GGCTCTGAC CTGTGAGCA ACAGTCATG GGCATTGTA TAAGACAAAC TATCTCACAC  
 TTCCCGAAAGT ACTATAGTTT ACGTGTGCAAT TTCTTCTATC CGGAAACAT ATTCTGTTG ATAGAGTGTG  
 6601 ATCGACAAAC CAATACAATC TAGCTGTTG GTTATGTTAG

**FIG.\_32G**

1 TTCGAGCTCG CCCGACATTG ATTATTGACT AGTTATCAAT TACGGGGTCA TTAGTTCAT A GCCCATATA GGAGTCCGC GTTACATAAC  
 AAGCTCGAGC GGGCTGTAAC TAAATAACTGA TCAATTATTA TCATTAGTTA ATGCCCCAGT AATCAAGTAT CGGGTATATA CCTCAAGGGC CAATGTATTG  
  
 101 TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAAAGCACCC CGGCCCATG ACGTCATAAA TGACCGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA  
 AATGCCATT ACCGGGGGA CGAAGTGGG GGTTGCTGGG GGGGGTAAC TGCAGTTATT ACTGCATACA AGGGTATCAT TGGGTATAC CCTGAAAGGT  
  
 201 TTGACGTCAA TGGGGAGT ATTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGT TAATATGCCA AGTACGCCC CTATTGACGT CAAATGACGGT  
 AACTGCAGT ACCAACCTCA TAATGCCAT TTGACGGGTAG TACTGGTACG TAGTTCACAT AGTACGGT TCATGCCA GTAACTGCCA GTTACTGCCA  
  
 301 AAATGGCCCG CCTGGCATTA TGGCCAGTAC ATGACCTTAT GGGAAGTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTAACG ATGGCTATGC  
 TTTACGGGC GGACCGTAAT ACGGGTATG TACTGGATAA CCCTGAAAGG ATGAAACCGTC ATGTAAGATGC ATAATCAGTA GCGATAATGG TACCACTACG  
  
 401 GGGTTTGCA GTACATCAAT GGGCGTGGAT AGCGGGTTGA CTCACGGGA TTCCAAAGTC TCCACCCCCAT TGACGTCAAT GGGAGTTGT TTGGCACCA  
 CAAAACCGT CATGTAGTTA CCCGGACCTA TGCCAAACT GAGTGGCCCT AAAGGGTCAG AGGTGGGTA ACTGCAGTTA CCCTCAAAACA AAACCGTGGT  
  
 501 AAATCAACGG GACTTTCCAA ATATGCTGAA CAACTCCGCC CCATTGACGC AAATGGGGGG TAGGGGTGTA CGGTGGGAGG TCTATAAG CAGAGCTCGT  
 TTAGTTGCC CTGAAAGGTT TTACAGGATT GTGAGGGGG GTGAACTGCG TTTACCGCC ATCCGCACAT GCCACCCCTC AGATATATTG GTCCTGAGCA  
  
 601 TTAGTGAACC GTCAGATCGC CTGGAGACGC CATCCACGCT GTTTGACCT CCATAGAAGA CACGGGACC GATCCAGCCT CGGGGGGG GAACGGGTGCA  
 AATCACTGG CAGCTAGCG GACCTCTGGC GTAGGTGGCA CAAAACGTGA GGTATCTCT GTGGCCCTGG CTAGGTGGA GGCGGGCC CTGGCACGTT  
  
 701 TTGGAAACGG GATTCCCCGT GCGAAGAGTG ACCTAAGTAC CGCCATATAGA GTCTATAGGC CCACCCCCCTT GGCTTCGTTA GAAACGGGGCT ACZATTAAATA  
 AACCTGGGC CTAAGGGGA CGGGTTCTCAC TGCATCTAG GCGGATATCT CAGATATCCG GGTGGGGAA CGAAGCAAT CTGGCCCGA TGTAAATTAT  
  
 801 CATAACCTTA TGTATCATAAC ACATACGATT TAGGTACAC TATAAGATAA CATCCACTTT GCCTTCTCT CCACAGGTGT CCACTCCAG GTCCAACCTGC  
 GTATGGAAAT ACATAGTATG TGTATGCTAA ATCCACTGTG ATATCTTATT GTAGGTGAAA CGGAAAGAGA GGTGTCACAA GGTTGAGGTC CAGGTGACG  
  
 901 ACCTGGTTTC TATCGATGAA ATTCCACCAT GGGATGGTCA TGTTATCATCC TTTTCTAGT AGCAACTGCA ACTGGAGTAC ATTCAAGATAT CCAGATGACC  
 TGGAGCCAG ATACTTAACG TAAAGTGGTA CCCTTACAGT ACATAGTGG AAAAGATCA TCGTTGACGT TGACCTCATG TAAGTCTATA GGTCTACTGG  
 1 M G W S C I L F L V A T G V H S D I Q M T  
 ^met ^Start VL  
 ^EcoRV

**FIG.- 33A**

1001 CAGTCCCGA GCTCCCTGTC CGCCTCTGTG GGCGATAGGG TCACCATCAC CTGCCGTGCC AGTCAGGATG TGTCACACTGC TGTAACCTGG TATCAAACAGA  
GTCACGGCT CGAGGACAG GCGGAGACAC CCGCATCCCC AGTGGTAGTG GACGGCACGG TCAGTCCTAC ACAGGTGACG ACATGGACC ATAGGTGTC  
25 Q S P S S L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K ^CDR-L1

1101 AACCAAGAAA AGCTCCGAAG CTTCTGATT ACTCGGCATC CTTCCCTCTAC TCTGGAGTCC CTTCTCGCTT CTCTGGTAGC GTTTCGGGA CGGATTTCAC  
TTGGTCCTT TGAGGCTTC TCGTCAGACG TCGGCCTCT GAAGACTAAA TGAGCCGTAG GAAGGAGATG AGACCTCAGG GAAGAGCAGA GAGACCATCG CCAAGGGCT GCCTAAAGTG  
59 P G K A P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T ^CDR-L2

1201 TCTGACCATC AGCAGTCTGC AGCCGGAGA CTTCCGAAC TATTACTGTC AGCAATCTTA TACTACTCCT CCCACGTTCTG GACAGGGTAC CAAGGGTGGAG  
AGACTGGTAG TCGTCAGACG TCGGCCTCT GAAGCCGTAG ATAATGACAG TCGTTAGAAC ATGATGAGGA GGGTGCAGC CTGTCCCAGT GTTCCACCTC  
92 L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E ^KpnI ^CDR-L3

1301 ATCAAACGAA CTGTCGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA TGAGGAGTTG AAATCTGGAA CTGCTCTGT TGTGTCGCTG CTGAATAACT  
TAGTTGCTT GACACCGACG TGGTAGACAG AAGTAGAAGG GCGGTAGACT ACTCGTCAAC TTAGACCTT GACGAAGACA ACACACGGAC GACTTATTGA  
125 I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F ^start human kappa

1401 TCTATCCAG AGAGGCCAA GTACAGTGGAA AGGTGGATAA CGCCCTCCAA TCGGGTAAC CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC  
AGATAGGGTC TCTCCGGTT CATGTCACCT TCCACCTATT GCGGGAGGT AGGCCATATGA GGGCCTCTC ACAGTGTCTC GTCCCTGTCTG TCCCTGTCTG  
159 Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T

1501 CTACAGCCCTC AGCAGCACCC TGACGCTGAG CAAAGCAGAC TAGGAGAAC ACAAAAGTCTA CGCCTGCAGA GTCACCCATC AGGGCCTGAG CTGCCCGTC  
GATGTCGGAG TCGTCGGG ACTGGGACTC GTTTCGTCTG ATGCTCTT TGTTTCAGAT GCGGACGCTT CAGTGGTAG TCCCGGACTC GAGGGGGCAG  
192 Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V

1601 ACAAAGAGCT TCAACAGGG AGAGTGTAA GCTTGGCCGC CATGGCCAA CTTGTTTATA ATGGTTACAA ATAAAGCAAT AGCATCACAA  
TGTTTCGCA AGTGTCCCC TCTCACATT CGAACGGGTG GTACCGGGT GAACAATAA CGTCAATATT TACCAATGTT TATTICGTTA TCGTAGTGT  
225 T K S F N R G E C O

1701 ATTTCACAAA TAAAGCATT TTTTCACTGC ATTCTAGTTCG TGGTTTGTCC AACTCATCA ATGATATCTTA TCATGTCGG ATCGGAATT AATTGGGCC  
TAAAGTGTTC ATTTCGTAAA AAAAGTGAAG TAAGATCAAC ACCAACAGG TTAGTAGTACATAAAT AGTACAGACC TAGCCCTAA TTAAGCCGGC

1801 AGCACCAGG CCTGAAATAA CCTCTGAAG AGGAACTTGG TTAGGTATCT TCTGAGGGG AAAGAACAG CTGTGAATG TGTGTCAGT AGGGTGTGGA  
TCGTGGTACG GGACTTATT GGAGACTTTC TCCTTGACCA ATCCATAGA AGACTCCGCC TTCTTGTC GACACCTAC ACACAGTCAA TCCCACACCT  
^ change from C to T, kill KpnI site

1901 AAGTCCCCAG GCTCCCCAGC AGCCAGAAGT ATGCCAAGCA TGCATCTCAA TTAGTCAGCA ACCAGGTGTG GAAAGTCCCC AGGCTCCCCA GCAGGGAGAA  
TTCAGGGTTC CGAGGGTTCG TCCGTTCTCA TACGTGTCTGT ACGTAGAGT AATCAGTGTG TGGTCACAC CTTTCAGGG TCCGAGGGT CTTCCGTCTIT

2001 GTATGCAAAG CATGCATCTC AATTAGTCAG CAACCATAGT CCCGCCCTA ACTCCGCCCA TCCGCCCT AACTCCGCC AGTTCCGCC ATTCTCCGCC  
CATACCTTTC GTACGTAGAG TTAATCAGTC GTTGETATCA GGGGGGGAT TGAGGGGG AGGGGGGG TCAAGGGGG TAAGAGGGGG

2101 CCATGGCTGA CTAATTTTTT TTATTATGC AGAGGCCGAG GCCGCCCTGG CCTCTGAGCT ATTCCAGAAG TAGTGGAGG GTCTTTTTGG AGGCCTAGGC  
GGTACCAACT GATTAATAAA AATTAATAGC TCTCCGGCTC CGGGGGAGCC GGAGACTC GA TAAGGTCTTC ATCACTCTC CGAAAAAAACC TCCGGATCCG

2201 TTTTGCAAA AGCTGTTAAC AGCTGGCAC TGGCGTGT TTACAACGT CGTGACTGGG AAAACCTGG CGTACCCAA CTTAATGCC TTGAGCACA  
AAACGTTT TCAGACAAATTG TCGAACCTGT ACCGGAGCA AAATGTTGCA GCACTGACCC TTTGGGACC GCAATGGTT GAATAGGGG AACGTCTGTGT

2301 TCCCCCTTC GCCAGCTGGC GTAATAGCGA AGAGGCCG ACCGATCGCC CTTCCCAACA GTTGGTAGC CTGAATGGCG AATGGGCCCT GATGGGTAT  
AGGGGGAAAG CGGTGCAACCG CATTATGGCT TCTCCGGGG TGGCTAGCG GAAGGGTTGT CAAGGCATCG GACTTACCGC TTACCGGGGA CTACGCCATA

2401 TTCTCTCTTA CGGATCTGTG CGGTATTCA CACCCATAC GTCAAAGCA CCATAGTACG CGCCCTGTAG CGGGCATTAA AGCCGATTA AGCCGGGG  
AAAGAGGAAT GCGTAGACAC GCCATAAAAGT GTGGGTATG CAGTTCTGT GTATCATGC GCGGACATC GCGGCCATAAT TCGGCCGCC CAACCCACCA

2501 TACGGCAGC GTGACCCGTA CACTTGCAG CGCCCTAGCG CCGCTCCTT TCCTTCCCTT CTCGCCACGT TCGCCGGCTT TCCCCGTCAA  
ATGGCGTCG CACTGGCGAT GTGAAACGGTC GGGGATCGC GGGGAGGAA AGCGAAAGAA GGGAGGGAA AGGGCCAGT

2601 GCTCTAAATC GGGGGCTCCC TTAGGGTTC CGATTAGTG CTTTACGGCA CCTCGACCCC AAAAAGCTG ATTTGGGTGA TGGGTCACTG AGTGGGCCAT  
CGAGATTAG CCCCGAGGG AAATCCAAAG GCTAAATCAC GAAATGCCGT GGAGCTGGG TTTTGAAC TAAACCCACT ACCAAGTGCA TCACCCGGTA

2701 CGCCCTGATA GACGGTTTT CGCCCTTGTCA CGTGGAGTC CACGTTCTT AATAGTGGAC TCTTGTCCA AACTGGAACA AACTCAACC CTATCTCGGG  
 GCGGAACTAT CTGCCAAAAA GCGGAAACT GCACCTCAG GTGCAAGAAA TTATCACCTG AGAACAAAGGT TTGACCTCTG TGTCAAGTGG GATAGAGCC  
  
 2801 CTATTCTTT GATTATAAG GGATTTGCC GATTTCGCC TATTGGTTAA AAAATGAGCT GATTTAACAA AAATTAAACG CGAATTAA CAAAATATTAA  
 GATAAGAAA CTAATATTAC CCTAAAGCCG CTAAGGCCG ATAACCAAT TTAACTCGA CTAAATTGTT TTAAATTGC GCTTAAATT GTTTTATAAT  
  
 2901 ACGTTTACAA TTTATGGTG CACTCTAGT ACAATCTGCT CTGATGCC ATAGTTAACG CAACTCGCT ATCGCTACGT GACTGGGTCA TGGCTGCGC  
 TGCAATGTT AAATACAC GTGAGACTCA TGTAGACGA GACTACGGCG TATCAATTG GTGAGGGCA TAGCGATGCA CTGACCCAGT ACCGACGCGG  
  
 3001 CCGACACCCG CCAACACCCG CTGACGCC CGTACGGGCT TGTCTGTC CGGCATCCGC TTACAGACAA GCTGTGACCG TCTCCGGAG CTGCAATGTT  
 GGCTGGGC GGTGTGGC GACTGCCGG GACTGCCGG GACTGCCGA ACAGACGAGG GCCGTAGGGC AATGTCGTG CGACACTGGC AGAGGCCCTC GACGTACACA  
  
 3101 CAGAGTTT CACCGTCATC ACCGAAACCGC GCGAGGGAGT ATTCTTGAAG ACGAAAGGGC CTCGTGATAC GCCTATTGTT ATAGGTTAAT GTCAATGATAA  
 GTCTCCAAA GTGGCAAGTAG TGGCTTGC CGCTCCGTCA TAAGAACTTC TGCTTCCCCG GAGCACTATG CGGATAAAA TATCCAATT CAGTACTATT  
  
 3201 TAATGGTTTC TTAGACGTC GGTGGCACTT TTGGGGAAA TGTGCGGGA ACCCCATT GTTATTTT CTAATAACAT TCAAATATGT ATCCGCTCAT  
 ATTACCAAAG AATCTGGAGT CCACCGTAA AAGCCCTTT ACACGGCCCT TGGGGATAAA CAAATAAAA GATTATGTA AGTTTATACA TAGGGAGTA  
  
 3301 GAGACAATAA CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTCCTCGT GTGCCCTTA TTCCCCTTT TGCGGCATT  
 CTCTGTATT GGGACTATT AGGAAGTTT TATACTTT TCCTTCTCAT ACTCATTAAGT TGAAAGCA CAGGGGAAT AAGGGAAAA AGCCGTAAA  
  
 3401 TGCCCTTCTG TTTTGCTCA CCCAGAAACG CTGGTGAAG TAAAGATGC TGAAGATCAG TTGGTGCAC GAGTGGTCA CATCGAACTG GATCTCAACA  
 ACGGAAGGAC AAAAACGAGT GGGCTTGC GACCACTTC ATTCTAGTC ACTCTAGTC AACCCACGTG CTCACCCAAAT GTAGCTGAC CTAGAGTTGT  
  
 3501 GCGGTAAGAT CCTGAGAGT TTTCGCCCCG AAGAACGFTT TCCAATGATG AGCACTTTA AAGTTCTGCT ATGTTCTGCC GATGATGACGC  
 CGCCATCTCA GGAACCTCA AAAGGGGGC TTCTTGAAA AGGTACTAC TCGTAAATT TTCAAGACGA TACACGGGC CATAATGGG CACTACTGGC  
  
 3601 CGGGCAAGAG CAACTCGGTG GCCGGAATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA  
 GCCCGTCTC GTTGGCCAG CGGGTATGT GATAAGAGTC TTACTGAAC AACTCATGAG TGGTCAGTGT CTTTCGTAG AATGCCTAAC GATCTGTCA

3701 AGAGAATTAT GCACTGCTGC CATAACCATG AGTGTATAACA CTGGGCCAA CTTACTCTG ACAACGATCG GAGGACGAA GGAGCTAACCG GCTTTTTTGC  
TCTCTTAATA CGTCAGCAG GTATGGTAC TCACTATGT GACGCCGGT GAATGAAGAC TGTGTGCTAGC CCTCTGGCTT CCTCGATTGG CGAAAAAACG

3801 ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA CGAGCGTGC ACCACGATGC CAGCAGCAAT  
TGTGTACCC CCTAGTACAT TGAGGGAAC TAGCAACCT TGGCCCTCGAC TTACTTCGGT ATGGTTGGT GCTGCAC TG TGCTCGTTA

3901 GGCAACAAAG TTGCGAAAC TATTAACCTT CGAAACTACTT ACTCTAGCTT CCCGGCAACA ATTAAAGAC TGGATGGGG CGGATAAGT TGCAGGACCA  
CGGTGTTGC AACCGTTTG ATAATGNAAC GCTTGTGAA TGAATGCAAC GGGCCGTTGT TAATTATCTG ACCTACCTCC GCCTATTICA ACCTCCCTGGT

4001 CTTCTGGCT CGGGCTTC GGCTGGCTGG TTATATGCTG ATAATCTGG AGCCGGTGAG CGTGGTATCAT TGCAGGACTG GGGCCAGATG  
GAAGACCGA GCGGGAAAGG CGGACCCGACC AAATTAACGAC TATTAAGAC TCGGCCACTC GCACCCAGAG CGCCATAGTA ACGTGTGAC CCCGGTCTAC

4101 GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGTTAA  
CATTCGGGAG EGCATAGCAT CAATAGATGT GCTGGCCCTC AGTCCGTTGA TACCTACTTG CTTATCTGT CTAGCGACTC TATCCACCGA GTGACTTAATT

4201 GCATTGGTAA CTGTCAAGACC AAGTTTACTC ATATATACTT TAGATTGAT TAAACTTCA TTTTAATT AAAAGGATCT AGGTAAAGAT CCTTTTGAT  
CGTAACCATT GACAGTCTGG TCCAATATGAG TATATATGAA ATCTAACTAA ATTGGAAAGT AAAAATAAA TTTCCTAGA TCCACTTCTA GAAAAGACTA

4301 AATCTCATGA CCAAATCCC TTACGTGAG TTTCGTTCC ACTGAGGCTC AGACCCCGTA GAAAAGATCA AAGGATCTC TTGAGATCCT TTGAGATCCT  
TTAGAGTACT GGTTTAGGG AATTGCACTC AAAAGCAAGG TGACTCGCAG TCTGGGCAT CTTTCTAGT TCCTAGAAG AACTCTAGGA AAAAAGACG

4401 GCGTAATCTG CTGCTTGCAA ACAAAAAAC CACCGCTACC AGGGGGTT TGTTTGCGG ATCAAGAGCT ACCAAACTCTT TTTCGGAAGG TAATCTGGCTT  
CGCATTAGAC GACGAACGTT TGTTTTTTG GTGGGATGG TCGGCCACCAA ACAAAACGGCC TAGTTCTCGA TGGTTGAGAA AAAGGCTTCC ATTGACCCGA

4501 CAGCAGGG CAGATACCAA ATACTGCTCT TCTAGTGTAG CCCTAGTTAG GCCACCAACTT CAAGAAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA  
GTCGTCGCG GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CGGTGGTGAAT GTTCTTGAGA CATCGTGGCG GATGTTGAGA GCGAGACGAT

4601 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTGT GTCTTACCGG GTGGGACTCA AGACGATAGT TACCGGATAA GGGCAGCGG TCGGGCTGAA  
TAGGACAATG GTCACCGACG ACGGTCAACCG CTTATCAGCA CAGAATGGCC CAACCTGACTA ATGGCTTATT CCGCGTGCCTAGT TCTGCTATCA AGCCCGACTT

4701 CGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCATTGAGAA AGCCACAGC TTCCCGAAGG  
GCCCCCAAG CACGTGTC GGGTCGAAACC TCGCTTGCTG GATGTGGCTT GACTCTATGG ATGTGCGACT CGTAACTCTT TCGGGGTGCG AAGGGCTTC

4801 GAGAAAGGGCG GACAGGTATC CGGTAAAGGG CAGGGTCTGGA ACAGGAGAGC GCACGAGGG GCACGAGGG GCTCCAGGG GGAAACGCTT GGTATCTTTA TAGTCCCTGTC  
CTCTTTCGGC CTGTCATAG GCCATTGCCG GTCCCCAGCC GTCTCCCTCG TCTCCCTCG CGTGTCTCC CGAAGGTCCC CCTTTCGGCA CCATMGAAT ATCAGGACAG

4901 GGGTTTCGCC ACCCTCTGACT TGAGCGTCA TTTTTGTGAT GCTCGTCAAGG GGGCGGGAGC CTATGGAAA AGGCCAGCAA CGCGGCCCTT TTACGGTTTC  
CCCAAAGCGG TGGAGACTGA ACTCGCAGCT AAAAACACTA CGAGCAGTC CCCCAGCTCG GATAACCTTT TGCGGTGTT GGCGCCGAAA ATGCCAAGG

5001 TGGCCTTTTG CTGGCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCT GATTCTGTGG ATAACCGTAT TACCGCTT GACTGAGCTG ATACCGCTCG  
ACCGAAAC GACCGAAMA CGACGGAAAG CGAGTGTACA AGMAAGGACG CAAATAGGGAA CTAAGACACC TATTGGCATA ATGGGGAAA CTCACTCGAC TATGGCGAGC

5101 CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGGCGAG GAAAGCGGAAG AGCGCCCAAT ACGAAACCG CCTCTCCCCG CGCGTTGGCC GATTCAATTAA  
GGCGTGGCT TGCTGGCTCG CGTCGCTCAG TCACTCGCTC CTTCGCCCTC TCGGGGTTA TGCGTTGGC GGAGGGGGC GCGAACCGG CTAAGTAATT

5201 TCCAGCTGGC ACGACAGGT TCCCGACTGG AAAGGGGGCA GTGAGCGCAA CGCAATTAAAT GTGAGTTACC TCACTCATTA GGCAACCCAG GCTTTACACT  
AGGTGACCG TGCTGTCCAA AGGGCTGACC TTTCGGCCGT CACTCGCGTT GCGTTAATTA CACTCAATGG AGTGAATCTT CCAGTAAAT CGTGGGTGCA

5301 TTATGCTTCC GGCTCGTATG TTGTGGAA TTGTGGGG ATAACAATT CACACAGGAA ACAGCTATGA CCATGATTAC GAATTAA  
AATACGAAGG CCGACCATAC AACACACCTT AACACTCGCC TATTGTTAAA GTGTGTCCTT GTGTGATACT GGACTAAATG CTTAATT

1 ATTGGAGCTC GCCGACATT GATTATTGAC TAGTTATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA TGGAGTCCG CGTTACATAA  
 TAAGCTCGAG CGGGCTGAA CTAATAACTG ATCAATAATT ATCATTAGT AATGCCCAAG TAATCAAGTA TCGGGTATAT ACCTCAAGGC GCAATGTATT  
  
 101 CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC CCCGCCCAT GACGTCAATA ATGACGTATG TCCCCTAGT AACGCAATA GGCACCTTCC  
 GAATGCATT TACCGGGGG ACCGACTGGC GGGTGTGG GGGGGGTA CTGCAAGTTAT TACTGCATAC AAGGGTATCA TTGGGTTAT CCCTGAAAGG  
  
 201 ATTGACGTCA ATGGTGGAG TATTACGGT AAACCTGGCCA CTGGGAGTA CATCAAGTGT ATCATATGCC AAGTACGCC CCTATGACCG TCAATGACGG  
 TAACTGCAGT TACCCACCTC ATAAATGCCA TTGACGGGT GAAACCGTCA TAGTATACGG TTGACGGGG GGATAACTGC AGTTACTGCC  
  
 301 TAAATGGCCC GCCTGGCATT ATGCCAGTA CATGACCTTA TGGGACTTTC CTACTGGCA GTACATCTAC GTATTAGTCA TCACATCTAC CATGGTGATG  
 ATTACCGGG CGGACCGTAA TACGGGTCAAT GTACTGAAT ACCCCTGAAGG GATGAAACCGT CATGTAGATG CATAATCAGT AGCGATAATG GTACCACTAC  
  
 401 CGGTTTGGC AGTACATCAA TGGGCGTGA TAGGGGTGG ACTCACGGGG ATTCCAAGT CTCCACCCCCA TTGACGTCAA TGGGAGTTG TTGACGGCACC  
 GCCAAAACCG TCATGTAGTT ACCCGCAACT ATCGCCAAAC TGAGTGCCTC TAAAGGGTCA GAGGTGGGT AACTGCAGTT ACCCTCAAAAC AAAACCGTGG  
  
 501 AAAATCAACG GGACTTTCCA AAATGCTGTA ACAACTCCGC CCCATTGACG CAAATGGGG GTAGGGTGT ACGGGGAG GTCTATATAA GCAGAGCTCG  
 TTTTAGTTGC CCTGAAAGGT TTACAGCAT TGTGAGGG GGGTAACTGC GTTACCGC CATCCGCACA TGCCACCCCTC CAGATATATT CGTCCTCGAGC  
  
 601 TTTAGTGAAC CGTCAGATCG CCTGGAGACG CCATCCACGC TGTGTTGAC CACAAACTGG AGGTATCTTC TGTTGGCCCTG GCTAGGTGG AGGGCCGGC CCTTGCCACCG  
 AAATCACTTG GGAGTCTGC GGACCTCTGC GGAGTCTGC  
  
 701 ATTGGAACGC GGATTCCCCG TGCCAAAGGT GACGTAAGTA CGCGCTTATAG AGTCTTACCG CCCACCCCT TGGCTTCGTT AGAACGGGC TACAATTAAAT  
 TAACCTGCG CCTAAGGGGC ACGGTTCTCA CTGCAATTCA CTGCAATTCA CTGCAATTCA ACCTGGGGAA ACCGAAGCAA TCTTGCGCCG ATGTTAAATTAA  
  
 801 ACATAACCTT ATGATCATCA CACATACGAT TTAGGTGACA CTATAGAATA ACATCCACTT TGCTTTCTC TCCACAGGTG TCCACTCCCA GTTCCAACCTG  
 TGTATTGGAA TACATAGTAT GTGTATGCTA AATCCACTGT GATATCTTAT TGTAGGTGAA ACGGAAAGAG AGGTGTCCAC AGGTGAGGT CCAGGGTGA  
  
 901 CACCTCGTT CTATCGATTG AATTCCACCA TGGGATGGTC ATGATCATC CTTTTCTAG TAGCAACTGC AACTGGAGC TACGGTGGG TTGAGCTGGT  
 GTGGAGCCAA GATAGCTAAC TAAAGGTGCT ACCCTACCG TACATAGTAG GAAAAAGATC ATCGTTGACG TTGACCTCGC ATGCGACTCC AAGTCGACCA  
 1 M G W S C I L F L V A T A T G A Y A E V Q L V  
 ^start signal peptide  
 ^met  
 ^start of heavy chain  
 ^BsiW1

**FIG.\_34A**

1001 GGAGTCTGGC GGTGCCAGG TGAGCCCTGG CGGTCTCACTC CGGTTCCTCC GTGCAGCTTC TGGCTTCACC ATTAGGGTT CTTGGATACA CTGGGTGGGT  
 CCTCAGACCG CCACGGGACC ACGTGGTCC CGCGACTGAG GCAAACAGGA CACGTGAAAG ACCGAAGTGG TAATCACCAA GAACTATGT GACCCACGCA  
 25 E S G G G L V Q P G G S L R L S C A A S G F T I S G S W I H W V R  
 ^CDR-H1

1101 CAGGCCCGG GTAAGGGCTT GGAATGGGTT GCCTGGATTG CTCCTTAGTG CGGCCTACT GACTATGCCG ATAGCGTCAA GGGCGTTTC ACTATAAGCG  
 GTCCGGGCC CATTCGGGA CCTAACCAA CGAACCTAAC GAGGAATATC GCCGGATGA CTGATACGGC TATGCAGTT CCCGGAAAG TGATATTGGC  
 58 Q A P G K G L E W V A W I A P Y S G A T D Y A D S V K G R F T I S A  
 ^CDR-H2

1201 CAGACACATC AAAAACACA GCCTACCTAC AAATGAAACAG CTTAAGAGCT GAGGACACTG CGGTCTTATA TTGTGCAAGA SAGGGGGCT TGTACTGGGT  
 GTCTGTGATG GTTTGGATG TTAACTTGTG TGATGGATG TTAACTTGTGAG GAACTGATAAT AACACGTTCT CTCCTGGCA ACATGACCCA  
 92 D T S K N T A Y L Q M N S L R A E D T A V Y Y C A R E G G L Y W V V  
 ^CDR-H3

1301 GTTCGACTAC TGGGGTCAAG GAACCCGGT CACCGCTTCC TCGGCCCTCCA CCAAGGGCCC ATCGGTCTTC CCCCTGGAC CCTCCCTCCA GAGGACCTCT  
CAAGGTGATG ACCCCAGTT CTTGGGACCA GTGGAGAGG AGCCGGAGGT GGTTCGGGG TAGCCAGAAAG GGGGACGGT GGAGGGGTT CTCTGGAGA  
 125 F D Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T S  
 "ApaI

1401 GGGGCCACAG CGGCCCTGG CTGCCTGGTC AAGGACTACT TCCCCGAAACC GGTGACGGTG TCGTGGAACT CAGGGCCCT GACCAGGGC GTGCACACCT  
 CCCCCGGTGC GCGGGGACCC GACGGACAG TTCCCTGATGA AGGGGGTTGG CCACGTGCCAC AGCACCTTGA GTCCGGGGGA CTGGCTGGGG CACGTGTGGA  
 158 G G T A A L G C L V K D Y F P V T V S W N S G A L T S G V H T F

1501 TCCCGGCTGT CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGGGTGGTG ACTGTGCCCT CTAGCAGCTT GGGCACCOAG ACCTACATCT GCAACGTGAA  
 AGGGCCGACA GGATGTCAGG AGTCCTGAGA TGAGGGAGTC GTCGCACCAC TGACACGGGA GATCGTCGAA CCCGTGGTC TGGATGTAGA CGFTGCACTT  
 192 P A V L Q S S G L Y S L S S V V T V P S S S L G T Q T Y I C N V N

1601 TCACAAGCCC AGCAACACCA AGGTGGACAA GAAAGTTGAG CCCAAATCT GTGACAAAC TCACACATGC CCACCGTCCC CAGCACCTGA ACTCCCTGGGG  
 AGTGTCTGGG TCGTTGGT TCCACCTGTT CTTCAACTC GGGTTTAGAA CACTGTTTG AGTGTGTAG GGTGGACGG GTCTGTGACT TGAGGGACCC  
 225 H K P S N T K V D K K V E P K S C D K T H T C P P C P A P E L L G

**FIG.\_34B**

1701 GGACCGTCAG TCTTCCTCTT CCCCAAGGACA CCCCTCATGAT CTCCCGGACC CTCAGGTCA CATGGTGGT GGTGGACGTG AGCCACCGAAG  
 CCTGGCAGTC AGAAGGAGAA GGGGGTTTT GGGTCTCTGT GGGAGTACTA GAGGGCTGG GGACTCCAGT GTACGCACCA CCACCTCGAC TCGGTGCTTC  
 258 G P S V F L F P P K P K D T L M I S R T P E V T C V V V D V S H E D

1801 ACCCTGAGGT CAAGTCAAC TGGTACGTGG ACGGCGTGG A GTGCCATAAT GCCAAGACAA AGCCGGGGAA GGAGGACTAC AACAGCACGT ACCGGGTGGT  
 TGGGACTCCA GTTCAAGTGT ACCATGCACC TGCGGCACCT CGACGTATT CGGTTCTGTT TCACGTCC CTCGTCATG TTGTCGTGCA TGGCCCCACA  
 292 P E V K F N W Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V

1901 CAGCGCTCTC ACCGTCCTGC ACCAGGA CTCG GCTGAATGGC AAGGAGTACA AGTGCAGGT CTCACAACAAA GCCCTCCAG CCCCATCGA GAAAACCATC  
 GTCGCAGGAG TGGCAGGACG TGGTCTGAC CGACCTACCG TCCCTCATGT TCACGTCC GAGGTGTT CGGGAGGTC GGGGGTAGCT CTTTGGTAG  
 325 S V L T V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I

2001 TCCAAGCCA AAGGGCAGCC CCGAGAACCA CAGGTGTACA CCTGCCCCC ATCCGGGAA GAGGTGACCA AGAACAGGT CAGCCTGACC TGCCTGGTCA  
 AGGTTTGGT TTCCCGTCGG GGCTCTTGGT GTCCACATGT GGGACGGGG TAGGGCCCTT CTCTACTGGT TGATGTTCTG GTCGGACTGG AGGGACCA  
 358 S K A K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K

2101 AAGGCTTCTA TCCCAGCGAC ATCGCCGG AGTGGGAGAG CAATGGGAG CCGGAGAAC ACTACAAGAC CACGCCCTCC GTGCTGGACT CCGACGGCTC  
 TTCCGAAGAT AGGTCGCTG TAGGGCACC TCACCCCTCTC GTTACCCGTC GGGCTCTGT TGATGTTCTG GTGGGAGG CACGACTGTA GGCTGGCGAG  
 392 G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S

2201 CTTCTCTCTC TACAGCAAGC TCACCGTGG CAAGGAGGG TGGCAGGAGG GGAACGTCTT CTCATGCTCC GTATGCCATG AGGCTCTGCA CAACCACTAC  
 GAAGAAGGAG ATGTCGTTG AGTGGACCT GTTCCTCGTCC ACCGGTCTGC CCTTGAGAA GAGTACGAGG CACTACGTAC TCCGAGACGT GTGGGTGATG  
 425 F F L Y S K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y

2301 ACCGAGAAGA GCCTCTCCCT GTCTCGGGT AAATGAGTGC GAGTCGACCT GCAGAAAGCTT GGCGCCOATG GCCCAACTTG TTTATTGCAAG  
 TGGCTCTCT CGGAGGGCA CAGAGGGCA TTTACTCAG CTGCGGGAT CTCAGCTGGA CGTCTTCGAA CGGTGAAAC AAATAACGTC  
 458 T Q K S L S L S P G K O

2401 CTTATAATGG TTACAAATAA AGCAATAGCA TCACAAATT CACAAATAAA GCATTTTT CACTGCATT TAGTTGGT TTGTCAAAC TCATCAATGT  
 GAATATTACCA ATGTTTATT TCAGTTATGT AGTGTAA GTGTTTATT CGTAAAAAA GTGACGTAAG ATCAACACCA AACAGGTTG AGTAGTTACA

2501 ATCTTATCAT GTCTGGATCG ATCAGGAAATT AATTGGCGCC AGCACCATGG CCTGAAATAA CCTCTGAAAG AGGAACATGG TAGGTACCT TCTGAGGGGG  
 TAGAATAGTA CAGACCTAGC TAGCCCTTAA TAAAGGCCGG TCCTGGTACCC GGACTTTATT GGAGACTTTC TCCTTGAAACC AATCATGGAG ACTCCGGC  
  
 2601 AAAGAACCAT CTGTGGAAATG TGCTGTCAATT AGGCTGTGGA AAGTCCCCAG GCTCCCCAG AGGCAGAAAT ATGCAAAGCA TGCACTCAA TTAGTCAGCA  
 TTCTGTGTA GACACCTTAC ACACAGTCAA TCCCACACCT TTCAAGGGGTG CGAGGGGTG TCGGTCTTCA TACGTTTGTG ACCTAGAGTT ATCAGTGT  
  
 2701 ACCAGGTGTG GAAAGTCCCCA AGGCTCCCCA AGCAGGCAGAA GTATGCAAAG CATGCATCTC AATTAGTCAG CAACCATAGT CCCGCCCTA ACTCCGCCA  
 TGGTCACAC CTTTCAGGGG TCCGAGGGGT CGTCCGGTCTT CATACTGTT GTACGTAGAG TTAAATCAGTC GTGGTATCA GGGGGGGAT TGAGGGGGGT  
  
 2801 TCCCCCCT AACTCCGCC AGTTCCGCC ATTCTCCGCC CCATGGCTGA CTAATTTTTTT TTATTATGC AGAGGCCAG GCGGCCCTGG CCTCTGAGCT  
 AGGGGGGG A TTAGGGGGG TCAAGGGGG TAAGAGGGGG GGTACCGACT GATTAAAAAA AATAAAATACG TCTCCGGTC CGGGGAGCC GGAGACTCGA  
  
 2901 ATTCCAGAAG TAGTGGAG GCTTTTTGG AGGGCTAGGC TTTTGCAAAA AGCTGTTAAC AGCTTGGCAC TGGCGTGT TTTACAACGT CGTGTACTGG  
 TAAGGTCTTC ATCACTCTC CGAAAAAACC TCCGGATCCG AAAACGTTT TCGACAAATTG TCGAACCGTG ACCGGACCA AAATGTTGCA GCACTGACCC  
  
 3001 AAAACCCCTGG CGTTACCAA CTTAATGCC TTGGCAGCACA TCCCCCCTTC GCCAGGTGGA GTAATAGCGA AGAGGCCGC ACCGATGCC CTTCCCAAACA  
 TTTTGGGACC GCAATGGTT GAATTAGGGG AACGTCTGTG AGGGGGAAAG CGGTCAACCG CATTATCGCT TCTCCGGCG TGGCTAGCCG GAAGGGTTGT  
  
 3101 GTTGCCTAGC CTGAATGGCG AATGGCCCT GATGGGTAT TTTCTCCTTA CGCATCTGT CGTATTTC CACCGCATAC GTCAAACCAA CCATAGTACG  
 AACGCATCG GACTTACCGC TTACCGGGAA CTACGCCATA AAAGAGGAAT GCGTAGACAC GCACATAAAAT GTGGCTATG CAGTTTCGTT GGTATCATGC  
  
 3201 CGCCCTGTAG CGGCATTA AGCGGGGG GTGTGGTGGT TAAGCGCAGC GTGACCGCTA CACTGGCGAT GTGAACGGTC GGGGGATCGC GGGGAGGAA AGCGAAAGAA  
 GGGGACATC GCGCGTAAT TCGGGCCGC CACACACCA ATGCGCGTGC CACTGGCGAT GTGAACGGTC GGGGGATCGC GGGGAGGAA AGCGAAAGAA  
  
 3301 CCCTTCTTT CTGGCCACGT TCGCCGGTT TCCCCGGTCAA GCTCTAAATC GGGGGCTCCC TTAGGGTTTC CGATTAGTG CTTACGGCA CTCGACCC  
 GGGAAAGAAA GAGGGGTGCA AGCGGGCGAA AGGGGCAAGTT CGAGATTAG CCCCCGAGGG AAATCCAAG GCTAAATCAC GAAATGCCGT GGAGCTGGGG  
  
 3401 AAAAAGCTTG ATTGGGTGA TGGTTCACTT AGTGGCCCAT CGCCCTGATA GACGGTTTTG CGGGCTTTGA CGTGGAGTC CACGGTCTTT ATATAGTGGAC  
 TTTTTGAAAC TAAACCCACT ACCAAGTGCATCACCTGGTA GCGGGACTAT CTGCCAAAAA GCGGGAAACT GCAACCTCAG GTGCAAGAAA TTATCACCTG

3501 TCTTGTTC AACTGGAACA ACACTCAACC CTATCTCGGG CTATTCTTT GATTATAAG GGATTTGCC GATTTCGGCC TATTGGTTAA AAAATGAGCT AGAACAAAGGT TTGACCTTGT TGTGAGTTGG GATAGGCC GATAAGAAA CTAACCAATT CCTAAACGG CTAAGCCGG ATAACCAATT TTACTCGA

3601 GATTAAACAA AAATTAAACG CGAATTAA CAAAAATTAA ACGTTACAA TTTATGGTG CACTCTAGT ACAATCTGGT CTGATGCCG ATAGTTAACGC CTAATTGTT TTAAATTGC GCTTAAATT GTCAAATGTT AAAATACAC GTGAGTCA TGTAGACGA GACTACGGCG TATCAATTGC

3701 CAACTCCGCT ATCGCTACGT GACTGGCTCA TGGCTGCC CCGCACCCG CCAACACCCG CTGACGCC CTGACGCC CTGACGGCT TGCTCTGGCT CGGCATCCGC GTTGAGGGGA TAGCGATGCA CTGACCCAGT ACCGACGCCGG GGCTGTGGGC GTTGTGGGC GACTGCCGG GACTGCCGG ACAGACGAGG GCCGTTAGGGCG

3801 TTACAGACAA GCTGTGACCG TCTCAGGGAG CTGGCATGTGT CAGAGGTTT CACCGTCAT ACCGAAACGC GCGAGGCAGT ATTCTTGAG ACGAAAGGGC AATGTCTGTT CGACACTGGC AGAGGCCCTC GACGTACACA GTCTCCAAA GTGGCAGTAG TGGCTTGCG CGCTCCGTO TAAGACTTC TGCTTTCCCG

3901 CTCGTGATAC GCCTATTATT ATTAGGTTAAT GTCATGATAA TAATGGTTT TTAGACGTC GGTGGCACTT TTCGGGAA TGTCGGGGAA ACCCCCTATT GAGCACTATG CGGATAAAA TATCCAATTA CAGTACTATT ATTACCAAAAG AATCTGCACTT CCACCGTAA AAGCCCTTT ACACGGCCCT AGGGATAAAA

4001 GTTTTATTCTT CTAAATACAT TCAAATATGTT ATCCGGCTCAT GAGACAATAA CCGTGATAAA TGCTCAATA ATATTGAAAGA AGGAAGAGTA TGAGTATTCA CAAATAAAA GATTATGTA AGTTTATACA TAGGGAGTA CTCTGTTATT GGGACTATT ACGAAGTTAT TATAACTTTT TCCTTCTCAT ACTCATAAATG

4101 ACATTTCCGT GTCCGCCCTTA TTCCCTTTT TGGCCATTI TGGCTTCCCTG TTTTTGCTCA CCCGAAACG CGGGTGAAG TAAAGATGC TGAAAGATCAG TGTAAGGGCA CAGGGGGAT AAGGGAAAAA ACGGCGTAAA AGGAAGGAC AAAACGAGT GGGTCTTGC GACCACTTC ATTCTCTAGC ACTTCTAGTC

4201 TTGGGTGCAC GAGTGGGTTA CATCGAAGCTG GATCTCAACA GCGGTAAAGAT CCTTGAGAGT TTGCCCCG AGAACGTTT TCCATTGATG AGCACTTTA AACCCACGTG CTCACCCAT GTAGCTTGAC CTAGAGTTGT CGCCATTCTA GGAACTCTCA AAAGGGGGC TTCTTGCAA AGGTTACTAC TCCTGAAAT

4301 AAGTTCTGCT ATGTGGCGG GTATTATCCC GTGATGACGC CGGGCAAGAG CAACTCGTC GCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC TTCAAGAGGA TACACCGGCC CATAATGGG CACTACTGGC GCCTGGTCTC GTTGAGCCAG CGGGTATGT GATAAGAGTC TTACTGAACC AACTCATGAG

4401 ACCAGTCACA GAAAGGCATC TTACGGATGG CATGACAGTA AGAGAAATTAT GCAAGTGC CATAACCATG AGTGTAAACA CTGGCGCCAA CTACTTCTG TGGTCAAGTGT CTTTTCGCTAG AATGCTTACG GTACTCTCAT TCTCTTAATA CGTCAACGACG GTATGGTAC ICATCTATGT GACGCCGGTT GAATGAAAGAC

4501 ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTGGC ACAACATGGG GGATCATGTA ACTGGCTTG ATCGCTTG ACCGGAGCTG AATGAAGCCA TGGTGTAGC CTCCTGGCT CCTCGATGG CGAAAAAACG TGTGTGACCC CCTAGTACAT TGAGCGAAC TAGCAAACCT TGGCCCTGAC TIACTCTGGT

4601 TACCAAAACGA CGAGGTGAC ACCACGATGC CAGCAGCAAT GGCAACAAACG TTGCGCAAAC TATTAACCTGG CGAACTACTT ACTCTAGCTT CCCGGAAACA  
 ATGGTTTGCT GCTGCCACTG TGGTGTACG GTCTGTCGTA CCCGTTGTTGC AACCGCTTGTG ATAATGACC GCTTGATGAA TGAGATGAA GGGCCGTTGT  
  
 4701 ATTATAGAC TGGATGGAGG CGGATAAAGT TCCAGGACCA CTTCTGGCT CGGCCCTTC GGCTGGCTGG TTATTGCTG ATAATCTGG AGCCGGTGAG  
 TAATTATCTG ACCTACCTCC GCCTATTCA ACCTCCTGGT GAAGACCGGA CGCCGGAAAGG CGAACCGACC AAATAACGAC TATTAAGACC TCGGCCCACTC  
  
 4801 CGTGGGTCTC GCGGTATCAT TGGAGCACTG GGGCCAGATG GTAAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGAACT ATGGATGAAAC  
 GCACCCAGAG CGCCATAGTA ACGTCGTGAC CCCGGTCTAC CAATTGGGAG GGCATAGCAT CAATAGATGT GTCGCCCTC AGTCCGGTGA TACCTACTTG  
  
 4901 GAAATAGACA GATGCTGAG ATAGGTGCTT CACTGATTA GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACT TAGATTGATT TAAAACCTCA  
 CTTTATCTGT CTAGCGACTC TATCCACGGA GTGACTAATT CGTAACCATT GACAGTCGG TTCAATGAG TATATATGAA ATCTAACTAA ATTITGAAGT  
  
 5001 TTTTTAAATT AAAAGGATCT AGGTGAAGAT CCTTTTGAT AATCTCATGA CCAAATCCC TTAAACGTGAG TTTTCGTTTC ACTGAGCGTC AGACCCCCGTA  
 AAAAAATTAAA TTTTCTAGA TCCACTCTTA GGAAAAACTA TTAGAGTACT GGTTTAGGG AATTGCACTC AAAAGCAAGG TGAETGCAG TCAGGGGCAAT  
  
 5101 GAAAAGATCA AAGGATCTTC TTGAGATCTT TTTTCTGC GGCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTAC AGGGTGGTT TGTTTGGCG  
 CTTTCTAGT TTCCTAGAAG AACTCTAGGA AAAAGACG CGCATTAGAC GACGAACGTT TTGTTTTTG GTGGCGATGG TGCCACCAA ACAAACGGCA  
  
 5201 ATCAAGAGCT ACCAACTCTT TTICCGAAGG TAACTGGCT CAGCAGAGGC CAGATAACAA ATACTGTCTT TCTAGTGTAG CGTAGTTAG GCCACCACTT  
 TAGTTCTCGA TGGTGAGAA AAAGGCTCC ATTGACCGAA GTCTGTCGCA GTCTATGGTT TATGACAGGA AGATCACATC GGCAATCAATC CGGTGGTGA  
  
 5301 CAAGAACTCT GTAGCACCGC CTACATACTT CGCTCTGCTA ATCCCTGTAC CAGTGGTGC TGCCAGTGGC GATAAGTGTG GTCTTACCGG GTTGGACTCA  
 GTTCTGAGA CATCTGGCG GATGTATGCA GCGAGACGAT TAGGACAATG GTCACCGAG ACGGTCACCG CTATTGAGCA CAGAATGGCC CAACCTGAGT  
  
 5401 AGACGATAGT TACCGATAA GGGCAGGGG TCGGGGTGAA CGGGGGTTG GTGCACACAG CCCAGCTGG AGCGAACGAC CTACACGAA CTGAGATACC  
 TCTGCTATCA ATGGCTTATT CGCGTCGCC AGCCCCACTT GCCCCCCCAAG CACGTGTGTC GGGTGAACC TGCTTGCTG ATGTGGCTT GACTCTATGG  
  
 5501 TACAGCGTGA GCATGAGAA AGCGCCACGG TTCCCGAAGG GAGAAAGGG GACAGGTATC CGGTAAAGCGG CAGGGTGGGA ACAGGAGAGC GCACGAGGGA  
 ATGTCGCACT CGTAACTCTT ICGGGTGCG AAGGGCTTCC CTCCTTTCCGC CTGTCATAG GCCATTCGCC GTCCCAGCC TGTCCTCTCG CTGCTCCCT  
  
 5601 GCTCCAGGG GAAACGCCT GGTATCTTA TAGTCTGTGTC GGTTTGCCTGCC ACCTCTGACT TGAGCGTCGA TTTTTGTGAT GCTCGTCAGG GGGGGGGAGC  
 CGAAGGTCCC CCTTGGGA CATAGAAAT ATCAGGACAG CCCAAAGGGG TGGAGACTGA ACTCGCAGCT AAAAACACTA CGAGCAGTCC CCCGGCTCG

5701 CTATGGAAA ACGCAGCAA CGGGCCCTTT TTACGGTTCC TGCCCTTTTG CTGGCCTTTT GCTCACATGT TCTTCCTGC GTTATCCCCT GATTCTGTGG  
GATACTTT TGCGTCGTT GCGCCGAAA AATGCCAAGG ACCGGAAAAC GACCGAAAGG AGAAAGGACG CAATAGGGGA CTAAGACACC

5801 ATAACCGTAT TACCGCCTT GAGTGAGCTG ATACCGCTCG CGCGAGCCGA ACCACCCAGC GCAGGGAGTC AGTGGCCAG GAAGGGGAG ACCGGCCAAAT  
TATTGGCATA ATGGGGAAA CTCACTCGAAC TATGGGAGC GGGGTGGCT TGCTGGCTCG CGTGCCTC TCACTCGCTC CTTGCCTTC TCGGGGTTA

5901 ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCACTAA TCCAACGTGGC ACGACAGGTT TCCCGACTGG AAAGGGGCA GTGAGCCAA CGCAATTAAAT  
TGGCTTTGGC GGAGGGGC CGCAACCGG CTAAGTAAAGGTT AGGTGACCC TGCTGTCAA AGGGCTGACC TTTGCCCCT CACTCGCGTT GCGTAAATTA

6001 GTGAGTTACC TCACTCATTA GGCACCCAG GCTTACACT TTATGCTTCC GGCTCGTATG TTGTGGAA TTGTGAGGG ATAACAATT CACACAGGAA  
CACTCAATGG AGTGAATTAAT CGGTGGGTG CGAATATGTGA AATACGAAGG CCGAGGATAC AACACACCTT AACACTCGCC TATTGTAAA GTGTGTCCCT

6101 ACAGCTATGA CCATGATTAC GAATAA  
TGTGATACT GGTACTAATG CTAAT

## **FIG.\_34G**

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LC Frequency	S	N	V	D	G	I	T	L	X
28	S 511	N 262	V 258	D 186	G 178	I 44	T 39	L 16	X 35
29	I 1	S 272	V 254	G 192	R 147	Y 70	T 29	D 28	X 45
30	S 612	N 849	K 176	G 169	R 86	I 81	D 29	K 17	A 17
31	S 849	N 676	T 496	R 170	F 47	I 29	D 25	G 18	X 53
32	Y 1055	N 128	W 97	F 77	S 61	D 40	R 25	X 69	
50	G 386	A 341	D 294	W 151	K 116	L 91	E 39	S 30	X 82
53	S 545	N 438	T 407	K 41	I 23	R 23	X 58		
91	Y 849	S 196	R 169	A 118	G 61	H 41	X 148		X 91
92	Y 362	G 356	N 248	S 193	D 114	L 94	T 64	H 43	I 38
93	S 738	N 346	Q 117	T 101	H 66	G 51	D 47	R 35	X 112
94	S 386	T 365	W 288	Y 172	L 14	F 79	A 46	P 43	V 1
96	L 264	Y 205	W 176	F 1	R 1	P 1	X 33	N 24	X 18
									40

**FIG. 35**

Residue	Natural Diversity	Diversity < DNA codon	% good	% covering
L1-28	SNVDGI	SNVDGI<RDT>	100%	94%
L1-29	ISVGN	ISVG<RKT>	100%	86%
L1-29		IV<RTT>	100%	56%
L1-30	SNKGRYTDAAE	SNKGGRRTDAAE<RVW>	92%	93%
L1-31	SNTRIDKG	SNTRDKGGAAE<RVW>	75%	95%
L1-31		SNTTRIIK<ANW>	100%	94%
L1-32	YNWFSDR	YNFSDATIV<DHT>	55%	88%
L1-32		YFS<THT>	100%	77%
L2-50	GADWKLES	GAWLSV<KBG>	83%	67%
L2-53	SNTKIR	SNT<AVC>	100%	90%
L3-91	YSRAGH	YSAD<KMT>	75%	74%
		YS<TMT>	100%	66%
L3-92	YGNSDLTHI	YNSDTIFAV<DHT>	67%	64%
		YNSDTA<DMC>	83%	62%
L3-93	SNQTHGDR	SNTGDA<RVT>	83%	80%
		SNTDYAFIV<DHT>	44%	76%
L3-94	STWYLFAPVI	STYLFAPVINDH<NHT>	75%	78%
		STYFIN<WHT>	83%	43%
L3-96	LYWFIRP	LYFPHS<YHT>	67%	52%
		LYFIHN<HWT>	67%	58%
		LFI<HTT>	100%	42%
		LLWR<YKG>	100%	47%
		YF<TWT>	100%	29%

**FIG. 36**

**Light Chain Designed Diversity**  
Diversity:  $\sim 2.9 \times 10^9$

**CDR-L1:** diversity  $\sim 7 \times 10^3$

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		R	R	V
				Y

**CDR-L2:** diversity = 18

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

**CDR-L3:** diversity  $\sim 2.3 \times 10^4$

91	92	93	94	96
KMT	DHT	DHT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	F	F	F	L
Y	I	I	H	P
	N	N	I	S
	S	S	L	Y
	T	T	N	
	V	V	P	
	Y	Y	S	
			T	
			V	
			Y	

**Light Chain Designed Diversity**  
Diversity:  $\sim 6.1 \times 10^8$

**CDR-L1:** diversity  $\sim 3.4 \times 10^3$

28	29	30	31	32
RDT	RTT	RVW	ANW	THT
D	I	D	I	F
G	V	E	K	S
I		G	N	Y
N		K	R	
S		N	S	
V		S	T	
		T	V	

**CDR-L2:** diversity = 18

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

**CDR-L3:** diversity  $\sim 1.0 \times 10^4$

91	92	93	94	96
KMT	DMC	RVT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	N	G	F	L
Y	S	N	H	P
	T	S	I	S
	Y	T	L	Y
			N	
			P	
			S	
			T	
			V	
			Y	

**FIG. 37**

**FIG. 38**

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Light Chain Designed Diversity					CDR-L1					
CDR-L3: diversity ~ $1.3 \times 10^3$					28	29	30	31	32	
91	92	93	94	96	RDT	RTT	RVW	RVW	DHT	
TMT	DMC	RVT	WHT	HTT	D	I	D	D	A	
S	A	A	F	F	G	V	E	E	D	
Y	D	D	I	I	I		G	G	F	
N	G	N	N	L	N		K	K	I	
S	N	S	S		S		N	N	N	
T	S	T			V		S	S	S	
Y	T	Y					T	T	T	
							V	V	V	

**FIG. 39**

## CDR-L2

50	53
DVK	AVM
A	N
G	K
L	R
S	S
V	T2
W	

## CDR-L3

91	92	93	94	96
NRT	NRT	RVM	NNK	TDK
C	C	A2	A	C
D	D	D	C	F
G	G	E	D	L
H	H	G2	E	W
N	N	K	F	Y
R	R	N	G	*
S	S	R	H	
Y	Y	S	I	
		T2	L	
			M	
			N	
			P	
			Q	
			R	
			etc	
			*	

\*Amber stop codon is encoded by the  
degenerate codon

**FIG. 40**

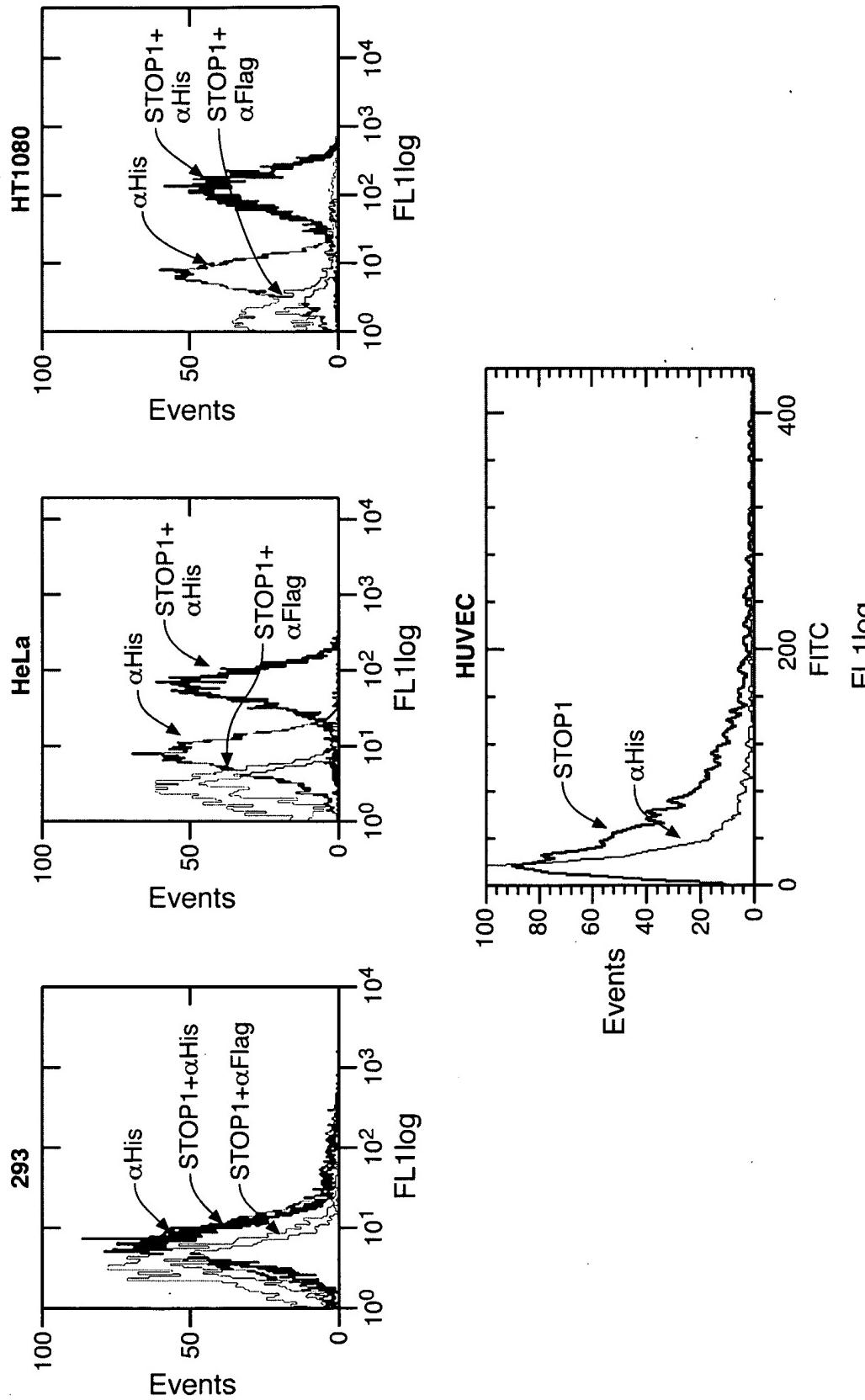
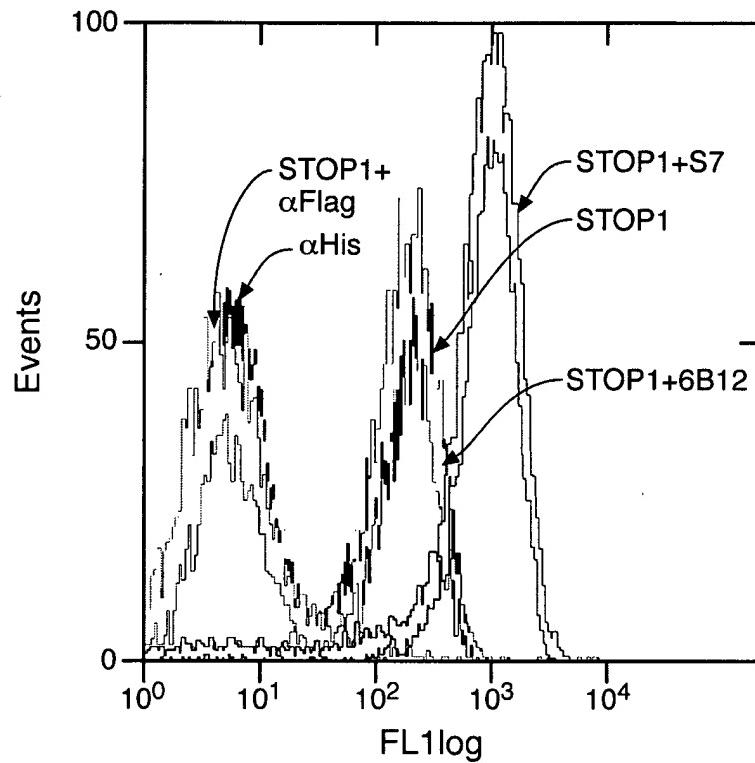
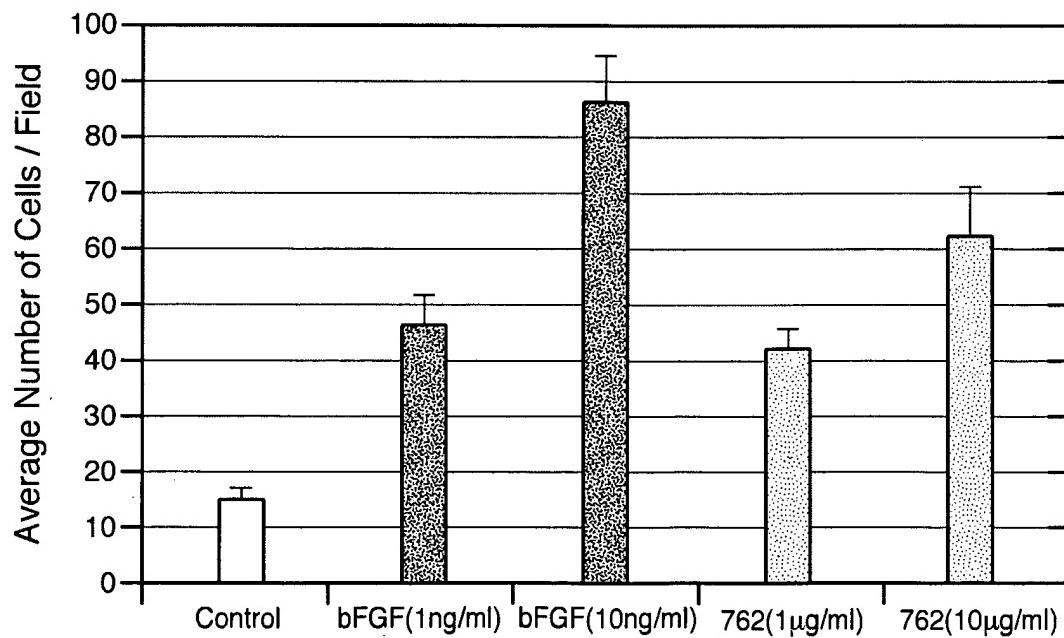


FIG. 41

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**FIG. 42****FIG. 43**

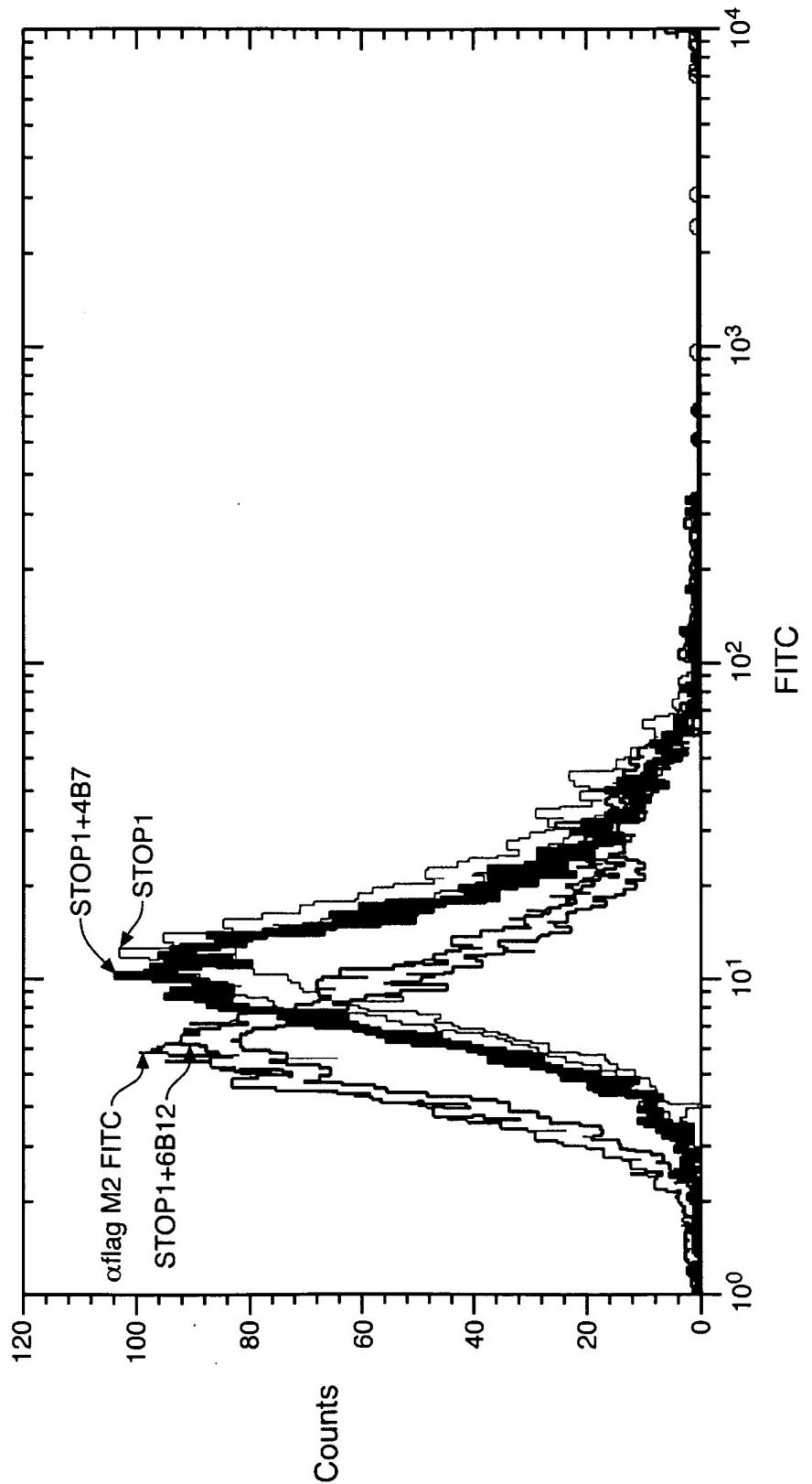
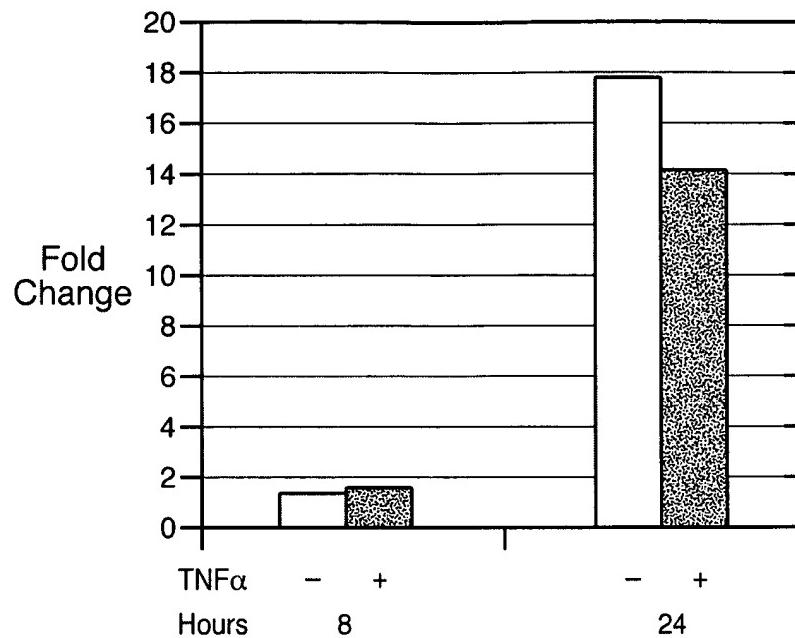


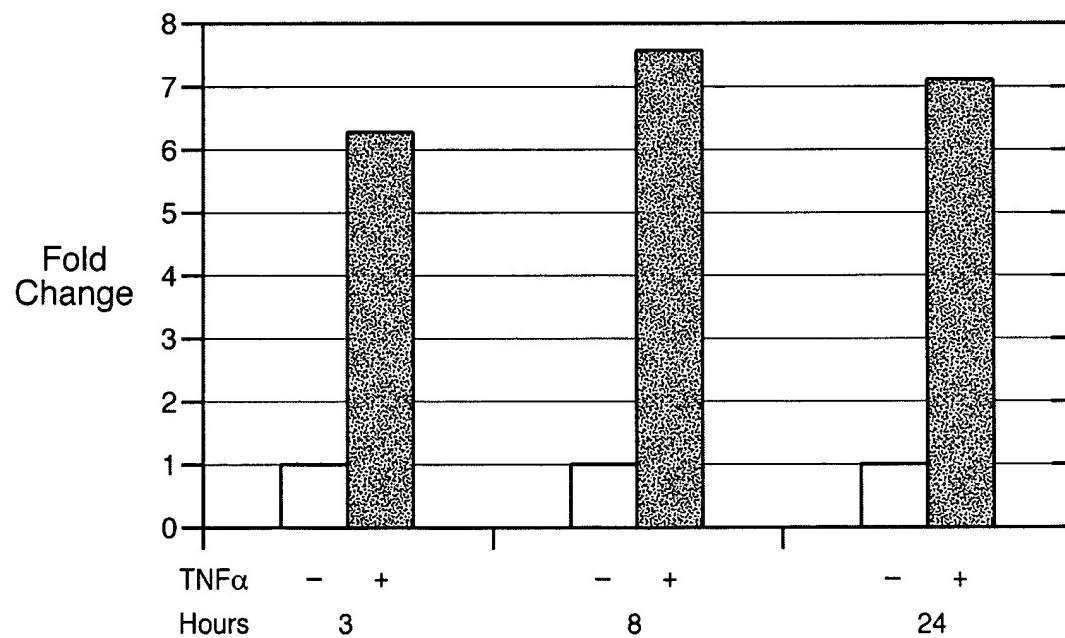
FIG. 44

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**FIG. 45A**



**FIG. 45B**